

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 03:55:57 ; Search time 267 Seconds  
(without alignments)  
9574.787 Million cell updates/sec

Title: US-10-088-092A-29

Perfect score: 487

Sequence: 1 ctgcttctctgtctgctt.....ggccaccacccgcctgtga 487

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqn23Sep04:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn1990s:\*
- 4: Geneseqn2000s:\*
- 5: Geneseqn2001as:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	100.0	487	5	Aaf77401 Human pho
2	308.6	63.4	883	3	Aaf73130 Mouse sec
3	308.6	63.4	883	5	Aaf77387 Murine cD
4	190.4	39.1	320	3	Aaf73117 Mouse sec
5	190.4	39.1	320	5	Aaf77374 Murine cD
6	144	29.6	180550	10	ADL13850 Osteoarth
7	108.8	22.3	1160	5	ABV22259 Human pro
8	108.8	22.3	1160	5	ABV28096 Human pro
9	108.8	22.3	1160	5	ABV23366 Human pro
10	108.8	22.3	1160	5	ABV29244 Human pro
11	108.8	22.3	1160	5	ABV23388 Human pro
12	108.8	22.3	1160	5	ABV25535 Human pro
13	108.8	22.3	1160	5	ABV29221 Human pro
14	107.2	22.0	435	10	ADL13848 Osteoarth
15	107.2	22.0	435	10	ADL13847 Osteoarth
16	107.2	22.0	779	10	ADL13849 Osteoarth
17	107.2	22.0	854	1	AAN91258 Nucleotid
18	107.2	22.0	854	6	ABL69731 Prostate
19	107.2	22.0	854	6	ABV94158 Breast ca
20	107.2	22.0	854	8	ACC46906 Human pho
21	107.2	22.0	854	10	ADB75500 Prostate

22	107.2	22.0	854	10	ADL13846
23	107.2	22.0	854	11	ADI131881
24	107.2	22.0	967	10	ADD18503
25	107.2	22.0	997	12	AAL52397
26	107.2	22.0	997	12	ADN03977
27	107.2	22.0	1028	10	ADL13851
28	107.2	22.0	1076	3	AAF15635
29	107.2	22.0	1116	2	AZ41274 Human pro
30	107.2	22.0	1156	12	ADO2611 Human sof
31	105.6	21.7	479	2	AAQ26372 PLA2 cDNA
32	101.4	20.8	375	10	ADF51390 Mutant hu
33	101.4	20.8	375	10	ADA61977 Human cDN
34	100	20.5	372	1	AAN97209 DNA enco
35	99.8	20.5	1016	6	ABL59517 Human pho
36	99.8	20.5	1016	10	ADB31301 Testoster
37	99.8	20.5	1016	10	ACC82789 Human pho
38	99.8	20.5	1399	12	ADH13785 Human ENZ
39	98.2	20.2	1014	2	AAQ81138
40	89.4	18.4	854	4	AAH23112 Osteoarth
41	86	17.7	778	8	ACC46913 Mouse pho
42	86	17.7	810	2	AAT48835 Mouse PLA
43	85.8	17.6	1828	2	AAQ81137 RPLA2-10
44	85.4	17.5	592	3	AA53269 Human pho
45	85.4	17.5	878	3	AA60878 Human sec

ALIGNMENTS

RESULT 1

AAF77401

ID AAF77401 standard; cDNA; 487 BP.

XX AAF77401;

XX 12-JUN-2001 (first entry)

XX Human phospholipase A2 (PLA2) cDNA.

Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnary;  
antiinflammatory; tranquiliser; antiasthmatic; antiallergic; trauma;  
antirheumatic; antiarthritic; septic shock; pancreatitis;  
adult respiratory distress syndrome; ARDS; bronchial asthma; human;  
allergic rhinitis; rheumatoid arthritis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 59..487

FT FT /\*tag= a

FT FT /product= "PLA2"

FT FT /note= "Phospholipase A2"

FT FT sig\_peptide 59..115

FT FT /\*tag= b

FT FT /label= Signal\_peptide

FT FT mat\_peptide 116..484

FT FT /\*tag= c

FT FT /label= Mature\_PLA2

FT FT /note= "Mature phospholipase A2"

XX WO200121775-A1.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-JP006344.

XX 21-SEP-1999; 99JP-00266616.

XX (SHIO ) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanaeaki K;

XX WPI; 2001-290432/30.



PN	WO2000121775-A1.
XX	
PD	29-MAR-2001.
XX	
PF	18-SEP-2000; 2000WO-JP006344.
XX	
PR	21-SEP-1999; 99JP-00266616.
XX	(SHIO ) SHIONOGI & CO LTD.
PA	Ishizaki J, Suzuki N, Hanasaki K;
PI	WPI: 2001-290432/30.
PX	P-FSDB; AAB81021.
DR	
XX	Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT	and screening drug candidates for treating associated diseases e.g.
PT	septic shock, adult respiratory distress syndrome and rheumatoid
PT	arthritis.
XX	
XX	Example 3; Page 41-42; 50pp; Japanese.
PS	
CC	This invention relates to human secretory phospholipase A2 (PLA2) protein
CC	and the gene encoding it. Inhibitors of phospholipase A2 have
CC	antibacterial; immunosuppressive; antiinflammatory; tranquilliser;
CC	vulbaratory; antiasthmatic; antiallergic; antirheumatic; and antiarthritic
CC	activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
CC	the diagnosis of PLA2 associated diseases e.g. septic shock, adult
CC	respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
CC	allergic rhinitis and rheumatoid arthritis. The present sequence
CC	represents cDNA encoding murine PLA2. The murine PLA2 gene sequence is
CC	used in the invention for the identification and characterisation of the
CC	human PUA2 gene
XX	
SQ	Sequence 883 BP; 212 A; 277 C; 220 G; 174 T; 0 U; 0 Other;
	Query Match            63.4%; Score 308.6; DB 5; Length 883;
	Best Local Similarity   80.3%; Pred. No. 2.4e-73;
	Matches 362; Conservative   0; Mismatches 89; Indels   0; Gaps   0;
QY	37 CCTCCTTCCTCCCCGCAACCTGGATGAATCTCCCACGTGCTGTGTTTGCCTTCCT 96

QY	37	CTCTCCCTTCCCGCAACCTCCGGATGAAATCTCCCCACGTCGTGTCTCTTTCCTCCT	Query Match	Score 190.4;	DB 3;	Length 320;
			39.1%			

Best Local Similarity 78.5%; Pred. No. 1.7e-41;  
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 146 AAGATGACAGGCAAGTCGCCCTGCAGTACACGACTATGGCTGTACTGGCGCATCGGT 205  
DB 5 AAGAGANGAGGGAACCTGCCCTGNAGTACATNACTATGGCTGTATTGGCGTTCGGT 64

QY 206 GGCTCCCACTGGCCGT-GGACCACTGACTGGTGGTCCAGCCGACGACTCTGCTA 264  
DB 65 GGCTCCCACTGGCCGTGGGAGCAACGATGGTGTTCATGCCCATGACTGCTGCTA 124

QY 265 CGGGGCTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324  
DB 125 TGGCCGCTGGAGAACCTGGCTGTGACCCCAAGCTGGAAAAGTACCTTCTCTATCAC 184

QY 325 CGAACGTGGCATTTCTGGCCGCGGAGGACACACCTGGCAGCGGCTGACCTGGGAGTGTGA 384  
DB 185 TCGAGACAAATCTTCTGTGTGGTAAACGGCTTGGCAGCGGCATACCTGCGAATGTGA 244

QY 385 CAAAGAGGCTGCCCTCTGCTTTGGCGGCAACTGGGCACTTACAAACCGCAATATGCCCA 444  
DB 245 CAA-AAAACCGCTCTCTGCTTTGGCGCAACTGAACTTACAAACCGCAANTATGCCCA 303

QY 445 TTATCCCAACAAGCTGT 461  
DB 304 CTACCCCAACAAGCTGT 320

RESULT 5  
ID AAF77374 standard; cDNA; 320 BP.  
XX AAF77374;  
XX AAF77374;  
DT 12-JUN-2001 (first entry)  
DE Murine cDNA encoding phospholipase A2 (PLA2).  
XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;  
KW antiinflammatory; tranquilizer; antiallergic; antiallergic; trauma;  
KW antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;  
KW adult respiratory distress syndrome; ARDS; bronchial asthma;  
KW allergic rhinitis; rheumatoid arthritis; ss.  
OS Mus musculus.  
XX WO200121775-A1.  
XX 29-MAR-2001.  
XX 18-SEP-2000; 2000WO-JP006344.  
XX 21-SEP-1999; 99JP-00266616.  
XX (SHIO ) SHIONOGI & CO LTD.  
XX Ishizaki J, Suzuki N, Hanasaki K;  
PI WPI; 2001-290432/30.  
XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of  
PT and screening drug candidates for treating associated diseases e.g.  
PT septic shock, adult respiratory distress syndrome and rheumatoid  
PT arthritis.  
XX Example 1; Page 38; 50pp; Japanese.  
XX This invention relates to human secretory phospholipase A2 (PLA2) protein  
CC and the gene encoding it. Inhibitors of phospholipase A2 have  
CC antibacterial; immunosuppressive; antiallergic; antiallergic; tranquilizer;  
CC vulnery; antiallergic; antiallergic; antirheumatic; and antiarthritic  
CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in  
CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult

CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,  
CC allergic rhinitis and rheumatoid arthritis. The present sequence  
CC represents murine cDNA encoding PLA2 (EC.3.1.1.4). The murine sequence is  
CC used in the invention for the identification and characterisation of the  
CC human PLA2 gene  
XX

Sequence 320 BP; 78 A; 91 C; 76 G; 70 T; 0 U; 5 Other;

Query Match 39.1%; Score 190.4; DB 5; Length 320;  
Best Local Similarity 78.5%; Pred. No. 1.7e-41;  
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 146 AAGATGACAGGCAAGTCGCCCTGCAGTACACGACTATGGCTGTACTGGCGCATCGGT 205  
DB 5 AAGAGANGAGGGAACCTGCCCTGNAGTACATNACTATGGCTGTATTGGCGTTCGGT 64

QY 206 GGCTCCCACTGGCCGT-GGACCACTGACTGGTGGTCCAGCCGACGACTCTGCTA 264  
DB 65 GGCTCCCACTGGCCGTGGGAGCAACGATGGTGTTCATGCCCATGACTGCTGCTA 124

QY 265 CGGGGCTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTCTCTGTGAG 324  
DB 125 TGGCCGCTGGAGAACCTGGCTGTGACCCCAAGCTGGAAAAGTACCTTCTCTATCAC 184

QY 325 CGAACGTGGCATTTCTGGCCGCGGAGGACACACCTGGCAGCGGCTGACCTGGGAGTGTGA 384  
DB 185 TCGAGACAAATCTTCTGTGTGGTAAACGGCTTGGCAGCGGCATACCTGCGAATGTGA 244

QY 385 CAAAGAGGCTGCCCTCTGCTTTGGCGGCAACTGGGCACTTACAAACCGCAATATGCCCA 444  
DB 245 CAA-AAAACCGCTCTCTGCTTTGGCGCAACTGAACTTACAAACCGCAANTATGCCCA 303

QY 445 TTATCCCAACAAGCTGT 461  
DB 304 CTACCCCAACAAGCTGT 320

RESULT 6  
ADL13850  
ID ADL13850 standard; DNA; 180550 BP.  
XX ADL13850;  
XX ADL13850;  
DT 06-MAY-2004 (first entry)  
DE Osteoarthritis-associated polymorphic nucleotide #382.  
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;  
KW joint space narrowing; osteophyte development; joint pain;  
KW osteoarthritis; SNP; single nucleotide polymorphism.  
XX Homo sapiens.  
XX WO2003054166-A2.  
XX 03-JUL-2003.  
XX 19-DEC-2002; 2002WO-US041225.  
XX 20-DEC-2001; 2001US-0342603P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Jones KA, Schafer A;  
XX WPI; 2003-559141/52.  
XX Determining susceptibility of an individual to joint space narrowing,  
PT osteophyte development and/or joint pain comprises identifying whether  
PT the individual has at least one polymorphism in a polynucleotide encoding  
PT a protein.  
XX Disclosure; SEQ ID NO 382; 297pp; English.





Db 594 TGTGTGAGTGTGATAGGCTGTGACCTGTTTGTGTAAGAACAGACCTACAATA 653  
QY 432 GCAATATATCCCATATATCCACAGCTGTGACCGGGCCACCGGCTGCTGA 487  
Db 654 AAAAGTACCAGTACTATTCATAAACAAGTGCAGAGGGAGCACCCCTGTTGCTGA 709

RESULT 10  
ABV29244  
ID ABV29244 standard; cDNA; 1160 BP.  
XX  
AC ABV29244;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 29235.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW Pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US005171.  
XX  
PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 6238; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

Query Match 22.3%; Score 108.8; DB 5; Length 1160;  
Best Local Similarity 55.5%; Pred. No. 3.1e-19;  
Matches 231; Conservative 0; Mismatches 182; Indels 3; Gaps 1;  
QY 75 TCGTGGTTCCTTTGGCTCTCTGGTGTGTCACCGGAACTGTTGAGTTGGGG 134  
Db 294 TGGCAGTGCATGATCTTTGGCTCTCTGTCAGGCGCCATGGGAATTTGGCAATTCACCA 353  
QY 135 TGATGATCGAAGATGACAGGCAAG---TCGGCCCTGCATACAGACTATCGCTT 191

Db 354 GAATGATCAAGTTGACACAGGAAAGGAGCGCACTCAGTTATGGCTTCTATGGTGCC 413  
QY 192 ACTCGGCATCGTGGTCCCACTGGCGGTGGACACAGACTGACTGTGTGTCACGCC 251  
Db 414 ACTGTGGCGTGGTGGGAGAGGATCCCCCAAGGATGCAACGGATCGCTGTGTCACTC 473  
QY 252 ACGACTGCTGCTACGGCGCTGTGAGAAAGCTGGGCTGTGAGCCCAAACTGAAAAGTATC 311  
Db 474 ATGACTGTGCTACAAACGCTCTGGAGAAACGTGAATGTGGCACCATAATTTCTGAGCTACA 533  
QY 312 TTTTCTGTCTAGGAAAGCTGGGATTTTCTGCGCGGACGAGACCACTGCCAGGGGTGA 371  
Db 534 AGTTAGCAACTCGGGAGCAGAAATCACCTGTGCAAAAACAGGACTCTCTGCAGAGTCAAC 593  
QY 372 CCTGCGAGTGTGCAAGAGGGCTGCCCTGTGCTTTCGCCGCAACCTGGGACCTACAACC 431  
Db 594 TGTGTGAGTGTGATAGGCTGTGCCACCTGTTTGTGTAAGAACAGACCACTACAATA 653  
QY 432 GCAATATATCCCATATTCACAAAGCTGTGACCGGGCCACCGGCTGCTGA 487  
Db 654 AAAAGTACCAGTACTATTCATAAACAAGTGCAGAGGGAGCACCCCTGTTGCTGA 709

RESULT 11  
ABV23388  
ID ABV23388 standard; cDNA; 1160 BP.  
XX  
AC ABV23388;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 23379.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW Pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US005171.  
XX  
PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 4251; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)









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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 05:01:22 ; Search time 59 Seconds  
(without alignments)  
5867.020 Million cell updates/sec

Title: US-10-088-092A-29

Perfect score: 487

Sequence: 1 cgcgtttcttctgtgcctt.....ggccaccgccctgtgta 487

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*\*

1: /cgn2\_6/prodata/1/ina/5A COMB.seq:\*\*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq:\*\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*\*  
5: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq:\*\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	107.2	22.0	854	4	US-09-023-655-1207
2	105.6	21.7	479	1	US-08-186-895-9
3	101.4	20.8	375	4	US-09-740-569-1
4	101.4	20.8	375	4	US-10-255-576-1
5	99.8	20.5	1016	4	US-09-220-132-17
6	98.2	20.2	1014	2	US-08-888-497-31
7	98.2	20.2	1014	3	US-09-362-230-31
8	98.2	20.2	1014	5	PCT-US94-07926-31
9	85.8	17.6	1828	2	US-08-888-497-29
10	85.8	17.6	1828	3	US-09-362-230-29
11	85.8	17.6	1828	5	PCT-US94-07926-29
12	85.4	17.5	878	4	US-09-855-486-26
13	64.8	13.3	4325	2	US-08-888-497-21
14	64.8	13.3	4325	3	US-09-362-230-21
15	64.8	13.3	4325	5	PCT-US94-07926-21
16	61.4	12.6	742	3	US-08-966-317-2
17	61.4	12.6	742	3	US-09-489-770-2
18	60.8	12.5	501	4	US-09-855-486-13
19	60.8	12.4	1233	4	US-09-855-486-13
20	60.2	12.4	496	4	US-10-140-002-533
21	58.4	12.0	562	4	US-09-023-655-1200
22	41.2	8.5	441	4	US-09-252-991A-14930
23	41.2	8.5	657	4	US-09-252-991A-15047
24	40.4	8.3	1686	4	US-09-252-991A-15047
25	40.4	8.3	1761	4	US-09-252-991A-5746
26	40.4	8.3	1890	4	US-09-252-991A-5746
27	38.8	8.0	1491	4	US-09-331-733-21

c

Query Match 22.0% ; Score 107.2 ; DB 4 ; Length 854 ;

28	38.4	7.9	1338	1	US-08-307-444A-8	Sequence 8, Appli
29	38.4	7.9	1338	1	US-08-587-389-8	Sequence 8, Appli
30	38.4	7.9	1368	1	US-08-307-444A-7	Sequence 7, Appli
31	38.4	7.9	1368	1	US-08-587-389-7	Sequence 7, Appli
32	38.4	7.9	1425	1	US-08-307-444A-6	Sequence 6, Appli
33	38.4	7.9	1425	1	US-08-587-389-6	Sequence 6, Appli
34	38	7.8	15328	2	US-08-888-497-33	Sequence 33, Appli
35	38	7.8	15328	3	US-09-362-230-33	Sequence 33, Appli
36	38	7.8	15328	5	PCT-US94-07926-33	Sequence 33, Appli
37	37.8	7.8	1425	1	US-08-307-444A-23	Sequence 23, Appli
38	37.8	7.8	1425	1	US-08-587-389-23	Sequence 23, Appli
39	37.2	7.6	825	1	US-08-312-870-6	Sequence 6, Appli
40	37.2	7.6	1428	1	US-08-014-723-3	Sequence 3, Appli
41	37.2	7.6	1428	1	US-08-014-723-4	Sequence 4, Appli
42	37.2	7.6	1428	1	US-08-110-011A-3	Sequence 3, Appli
43	37.2	7.6	1428	1	US-08-110-011A-4	Sequence 4, Appli
44	37.2	7.6	1491	1	US-08-312-870-2	Sequence 2, Appli
45	37.2	7.6	1680	1	US-08-014-723-13	Sequence 13, Appli

## ALIGNMENTS

RESULT 1  
US-09-023-655-1207  
; Sequence 1207, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1207:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 854 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g190888  
; US-09-023-655-1207



Qy	173	TACACGACTATGGCTGTTACTGCGGCAATCGTGGCTCCCACTGGCCGGTGGACCAACT	232
Db	61	TATGGCTTCTAGCGTGGCACTGTGGGTGGCAGAGATCCCCAAAGATGCAACG	120
Qy	233	GACTGTTGTGTCACGCCACGACTGCTGTCTACGGGGTCTGGAGAGCTGGGCTGTGAG	292
Db	121	GATCGTGTGTGTCACATCATGACTGTGTTGCTACAAACGTCTGGAGAAACGTGATGTGC	180
Qy	293	CCCAACTCGAAAGATATCTTTTCTCTGTACGCGAACGTGGCATTTTCTGCCCGCCAGG	352
Db	181	ACCAATTTCTGAGCTCAAGTTTAGCACTCGAAGAGCAATACCTGTGCAAAACAG	240
Qy	353	ACCACCTGCCAGCGCTCACTGCGAGTGTGACAAGAGGGCTGCCTCTCTCTTCGCCGC	412
Db	241	GACTCTGTGAGAAAGTCAACTGTGTGAGTGTGATAAGGCTGTGCACTGTTTGTCTAG	300
Qy	413	AACTGGGACCTTACAACCGGAATATGCCCATTTATCCCAACAGTGTGCACCGGGCC	472
Db	301	AACAGAGACCTTACATAAAGTACAGTACTATTCCCAATAAACACTCGAGGGAGC	360
Qy	473	ACCCGCCCTGCTGA	487
Db	361	ACCCCTCGTTGCTGA	375

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RESULT 4
US-10-255-576-1
; Sequence 1, Application US/10255576
; Patent No. 6767538
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTI-BACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THEREFOR
; FILE REFERENCE: 5986/1ES17US1
; CURRENT APPLICATION NUMBER: US/10/255,576
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/740,569
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-255-576-1

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Qy	413	AACCTGGGACCTACAAACCCCAATATGCCCATTTATCCCAACAGCTGTGCAACCGGGCC	472
Db	301	AACAAGAAGACCTACCAATAAAAAAGTACCAGTACTATTCCAAATAACACTGCAGAGGAGC	360
Qy	473	ACCCGGCCCTGCTGA	487
Db	361	ACCCCTGTTGCTGA	375
RESULT 5			
US-09-220-132-17			
; Sequence 17, Application US/09220132			
; Patent No. 650607			
; GENERAL INFORMATION:			
; APPLICANT: Shyjan, Andrew W.			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSES			
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROST			
; FILE REFERENCE: 07334-074001			
; CURRENT APPLICATION NUMBER: US/09/220,132			
; PRIORITY FILING DATE: 1998-12-23			
; PRIOR APPLICATION NUMBER: US 60/079,303			
; PRIOR FILING DATE: 1998-03-25			
; PRIOR APPLICATION NUMBER: US 60/068,821			
; PRIOR FILING DATE: 1997-12-24			
; NUMBER OF SEQ ID NOS: 191			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 17			
; LENGTH: 1016			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-220-132-17			
Query Match 20.5%; Score 99.8; DB 4; Length 1016;			
Best Local Similarity 54.5%; Pred. No. 1.1e-19;			
Matches 222; Conservative 0; Mismatches 182; Indels 3; Gaps 1.			
Qy	82	GTTCCTTTGCTCCTCGTGGCTCTGGTFCACGGGAACCTGTTTCAGTTTGGGGTGATGAT	141
Db	159	GTTCCTGGCTTGTAGTGTGCTGCTGTGCAAGAGGCTTCTGAGCACTAAATCAATGAT	218
Qy	142	CGAAGAGATGACAGGCAAGTCCGCCCTG---CAGTACAAGACTATGCGCTGTATTCTGCGG	198
Db	219	CGAAGAGTGCACAGGGAAGAACGCCCTGACAACTACGGCTTCTACGGCTGTTACTGCGG	278
Qy	199	CATCGTGGTCCCATGCGCGGTGACACAGACTGACTGTGCTGCACGCCCAAGACTG	258
Db	279	CTGGGCGGCGCAGGAACCCCAAGATGCAATGCTGTTGTTGGGCGCATGACCA	338
Qy	259	CTGCTACGGCGCTCGAGAGCTGGGCTGTGAGCCCAAACTGAAAGATATCTTTTCTC	318
Db	339	CTGCTATGGCGCGGTGAGAGAGGCTGCAACATTCGCACACAGTCTTACAATACAG	398
Qy	319	TGTCAGCGAACGTGGCATTTTCTGCGCGGCAGGACCACTGCCAGCGGTGACCTGCGA	378
Db	399	ATTTCGGTGGGCGTGGTCACTTCCAGCCGGGCCCTTCTGCCATGTGAACCTCTGTGC	458
Qy	379	GTGTGACAGAGGGCTGCCCTCTGCTTTCGCGGCAACCTGGGCACTTACAAACCGCAATA	438
Db	459	CTGTGACCGGAAGCTCGTCTACTCGCTCAAGAGAAACCTACGGAGCTACAAACCCACAGTA	518
Qy	439	TGCCCATATTCCCAACAAGCTGTGCAACCGGGCCCAACCCGCCCTGTCT	485
Db	519	CCAAATCTTTCCCAACAATCTCTGCTCCTAGGCTCCCCAGCGAGCT	565





STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 233..643  
US-08-888-497-29

Query Match 17.6%; Score 85.8; DB 2; Length 1828;  
Best Local Similarity 52.9%; Pred. No. 1.8e-15;  
Matches 208; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

QY 82 GTTCCTTTGCCCTCGCTGGTGGCTCTGTGTCACCGGGAACCTGGTTTCAGTTTGGGGTGATGAT 141  
DB 259 GTTCCTGGCTTGAGTGTGCTGCACTCCAGGGGGCTTGCTAGAACTGAAGTCCATGAT 318  
QY 142 CGAGAGATGACAGGCAAGTCCGCTCGAGTACAA---CGACTATGGCTGTACTGCGG 198  
DB 319 TGAGAGGTGACTGGGAAGATGCCGTAAAGAACTATGGCTTCTAGCGTGTCTACTGTGG 378  
QY 199 CATCGTGGCTCCCACTGGCGGCTGGACAGACTGCTGGTCCACGCCACGACTG 258  
DB 379 CTGGGCGGCCACCGGACCCCTTAAGATGGCATGTGTCGTGTCGATGACACCG 438  
QY 259 CTGCTAGGGGCTGAGAGAGCTGGCTGTGAGCCCAACTGGAAGTATCTTTCTC 318  
DB 439 TTGTTATGGGCTACTGGAGGAGAAACACTGTGCCATCCGACCCAGTCTATGACTACAG 498  
QY 319 TGTGACGAGAGCTGGGCAATTTCTGGCGGCGGACGACCTCCAGCGGCTGACCTGCGA 378  
DB 499 ATTACACAGGACTTAGTCTATCTCGAACACGACTCTTCTGTCAGTGAGSCTTTGTGC 558  
QY 379 GTGTGACAGAGGCTGCGCTCTGTCTTTCGCGCAACCTGGGCACTTACAAACGCAATA 438  
DB 559 TTGTGACCGGAGCTGTCTACTGCTGAGGAGAAACCTCTGAGTTACAAACCGCTTTTA 618  
QY 439 TGCCCATTTATCCCAACAAAGTGTGACCGGGCC 471  
DB 619 CCAGTATTACCCCAACTTCTCTGCTAAATGTCC 651

RESULT 10  
US-09-362-230-29  
Sequence 29, Application US/09362230  
Patent No. 6352849  
GENERAL INFORMATION:  
APPLICANT: Tischfield, Jay A.  
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
ADDRESS: Russell PA  
STREET: 200 East Broward Boulevard  
CITY: Fort Lauderdale  
STATE: FL  
COUNTRY: USA  
ZIP: 33301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/362,230  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/888,497  
FILING DATE:

APPLICATION NUMBER: US 08/097,354  
FILING DATE: 26-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-5  
TELEPHONE: 305-527-2498  
TELEFAX: 305-527-4996  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1828 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 233..643  
US-09-362-230-29

Query Match 17.6%; Score 85.8; DB 3; Length 1828;  
Best Local Similarity 52.9%; Pred. No. 1.8e-15;  
Matches 208; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

QY 82 GTTCCTTTGCCCTCGCTGGTGGCTCTGTGTCACCGGGAACCTGGTTTCAGTTTGGGGTGATGAT 141  
DB 259 GTTCCTGGCTTGAGTGTGCTGCACTCCAGGGGGCTTGCTAGAACTGAAGTCCATGAT 318  
QY 142 CGAGAGATGACAGGCAAGTCCGCTCGAGTACAA---CGACTATGGCTGTACTGCGG 198  
DB 319 TGAGAGGTGACTGGGAAGATGCCGTAAAGAACTATGGCTTCTAGCGTGTCTACTGTGG 378  
QY 199 CATCGTGGCTCCCACTGGCGGCTGGACAGACTGCTGGTCCACGCCACGACTG 258  
DB 379 CTGGGCGGCCACCGGACCCCTTAAGATGGCATGTGTCGTGTCGATGACACCG 438  
QY 259 CTGCTAGGGGCTGAGAGAGCTGGGCTGTGAGCCCAACTGGAAGTATCTTTCTC 318  
DB 439 TTGTTATGGGCTACTGGAGGAGAAACACTGTGCCATCCGACCCAGTCTATGACTACAG 498  
QY 319 TGTGACGAGAGCTGGGCAATTTCTGGCGGCGGACGACCTCCAGCGGCTGACCTGCGA 378  
DB 499 ATTACACAGGACTTAGTCTATCTCGAACACGACTCTTCTGTCAGTGAGGCTTTGTGC 558  
QY 379 GTGTGACAGAGGCTGCGCTCTGTCTTTCGCGCAACCTGGGCACTTACAAACGCAATA 438  
DB 559 TTGTGACCGGAGCTGTCTACTGCTGAGGAGAAACCTCTGAGTTACAAACCGCTTTTA 618  
QY 439 TGCCCATTTATCCCAACAAAGTGTGACCGGGCC 471  
DB 619 CCAGTATTACCCCAACTTCTCTGCTAAATGTCC 651

RESULT 11  
PCT-US94-07926-29  
Sequence 29, Application PC/TUS9407926  
GENERAL INFORMATION:  
APPLICANT: Tischfield, Jay A.  
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
ADDRESS: Russell PA  
STREET: 200 East Broward Boulevard  
CITY: Fort Lauderdale  
STATE: FL  
COUNTRY: USA  
ZIP: 33301





COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 26-JUL-1993  
APPLICATION NUMBER: US/08/888,497  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/06/651,405  
FILING DATE: 26-JUL-1993  
APPLICATION NUMBER: US/08/097,354  
FILING DATE: 26-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4325 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 722..1195  
US-08-888-497-21

Query Match 13.3%; Score 64.8; DB 2; Length 4325;  
Best Local Similarity 53.5%; Pred. No. 3.8e-09;  
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;

QY 132 GGGTGATGATCGAGAGATGACAGGCAAGTCGCGCTGCAGTACACGACTATGCTGT 191  
DB 825 GGNATGTCACACATCACGGGCGGAGGCTTCTTCTTATTACGATATGCTGT 884  
QY 192 ACTGCGGCATCGGTGCTCCACTGCGCGGTGGACGACTGCTGCTGCCAGCCC 251  
DB 885 ACTGTGGCTTGGGGCCGAGGATCCCTGTGGACCCACAGACAGTGTCTGGGCTC 944  
QY 252 AGACTGCTGTACGGGCTGTGGAGAGCTGGCTGTGAGCCCAACTGGAAAGTATC 311  
DB 945 ATGACTGTTGTACCAACAAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCTATC 1004  
QY 312 TTTTCTCTGTCAGCAACGTTGGCATTTTCTG-----CGCGGCGGAGGACCACT 359  
DB 1005 AGTTGCCATTGTCAACGGGACCGTGACCTGTGGATGCACCATGGTGGGCTGTTGT 1064  
QY 360 GCCAGCGGCTGACCTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTGCCGCCAACCTGG 419  
DB 1065 GCGGGCAGAAAGCCTGTGAGTGTGACAAACTGTGTACTGCTTCAAGGAGAACCTGG 1124  
QY 420 GCACCTACAA 429  
DB 1125 CCACCTACGA 1134

RESULT 14  
US-09-362-230-21  
Sequence 21, Application US/09362230  
Patent No. 6352849  
GENERAL INFORMATION:  
APPLICANT: Tischfield, Jay A.  
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
SEQUENCE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
ADDRESSEE: Russell PA  
STREET: 200 East Broward Boulevard  
CITY: Fort Lauderdale  
STATE: FL  
COUNTRY: USA  
ZIP: 33301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/362,230  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/888,497  
FILING DATE:  
APPLICATION NUMBER: US/08/097,354  
FILING DATE: 26-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4325 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 722..1195  
US-09-362-230-21

Query Match 13.3%; Score 64.8; DB 3; Length 4325;  
Best Local Similarity 53.5%; Pred. No. 3.8e-09;  
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;  
QY 132 GGGTGATGATCGAGAGATGACAGGCAAGTCGCGCTGCAGTACACGACTATGCTGT 191  
DB 825 GGNATGTCACACATCACGGGCGGAGGCTTCTTCTTATTACGATATGCTGT 884  
QY 192 ACTGCGGCATCGGTGCTCCACTGCGCGGTGGACGACTGCTGCTGCCAGCCC 251  
DB 885 ACTGTGGCTTGGGGCCGAGGATCCCTGTGGACCCACAGACAGTGTCTGGGCTC 944  
QY 252 AGACTGCTGTACGGGCTGTGGAGAGCTGGCTGTGAGCCCAACTGGAAAGTATC 311  
DB 945 ATGACTGTTGTACCAACAAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCTATC 1004  
QY 312 TTTTCTCTGTCAGCAACGTTGGCATTTTCTG-----CGCGGCGGAGGACCACT 359  
DB 1005 AGTTGCCATTGTCAACGGGACCGTGACCTGTGGATGCACCATGGTGGGCTGTTGT 1064  
QY 360 GCCAGCGGCTGACCTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTGCCGCCAACCTGG 419  
DB 1065 GCGGGCAGAAAGCCTGTGAGTGTGACAAACTGTGTACTGCTTCAAGGAGAACCTGG 1124  
QY 420 GCACCTACAA 429  
DB 1125 CCACCTACGA 1134  
RESULT 15  
PCT-US94-07926-21  
Sequence 21, Application PC/TUS9407926  
GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ruden Barnett, McClosky, Smith, Schuster &  
ADDRESSEE: Russell PA  
STREET: 200 East Broward Boulevard  
CITY: Fort Lauderdale  
STATE: FL  
COUNTRY: USA  
ZIP: 33301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07926  
FILING DATE: 15-JUL-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/097,354  
FILING DATE: 26-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4325 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 722..1195  
PCT-US94-07926-21

Query Match 13.3%; Score 64.8; DB 5; Length 4325;  
Best Local Similarity 53.5%; Pred. No. 3.8e-09;  
Matches 166; Conservative 0; Mismatches 132; Indels 12; Gaps 1;  
QY 132 GGGTATGATCGAGAGATGACAGGCAAGTCGGCCCTGCAGTACACAGACTATGGCTGT 191  
DB 825 GGATGGTCAAAACATACACGGGGCGCAGCGCTTCTCTCTATTACGGATATGGCTGT 884  
QY 192 ACTGGCGGATCGGTGGCTCCCACTGGCGGTGGACAGACTGCTGGTGTGCCACGCC 251  
DB 885 ACTGTGGCTTGGGGGCCAGGGATCCCTGTGGACGCCACAGACAGTGTCTGGGCTC 944  
QY 252 AGACTGTGTCTACGGGCGTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATC 311  
DB 945 ATGACTGTGTGTACCAAGCTTAAAGGAATATGGTGCAGCCCATCTTGAATGCCTATC 1004  
QY 312 TTTTCTCTCAGCGAAGTGGCATTTCTG-----CGCGGCGAGGACCACT 359  
DB 1005 AGTTTGCCATTGTCAACGGGACCGTGACCTGTGGATGCACCATGGTGGCGGCTGTGT 1064  
QY 360 GCCAGCGGTGACCTGCCAGTGTGACAAGAGGGTGCCTCTGTCTTTGCCGCCAACCTGG 419  
DB 1065 GCGGGCAGAAAGCTGTGAGTGTGACAAACTGTCTGTGTCTCTCAAGGAGAACCTGG 1124  
QY 420 GCACCTACAA 429  
DB 1125 CCACCTACGA 1134

Search completed: November 13, 2004, 06:11:26  
Job time : 60 secs

***This Page Blank (uspto)***

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	107.2	22.0	22.0	854	9	US-09-969-708-597	Sequence 597, Appl
2	107.2	22.0	854	10	US-09-865-866-3	Sequence 3, Appl	Sequence 597, Appl
3	107.2	22.0	854	15	US-10-203-823-324	Sequence 324, Appl	Sequence 324, Appl
4	107.2	22.0	854	15	US-10-102-544-1758	Sequence 1758, A	Sequence 1758, A
5	107.2	22.0	854	15	US-10-007-936A-149	Sequence 149, Appl	Sequence 149, Appl
6	107.2	22.0	854	15	US-10-172-118-465	Sequence 465, Appl	Sequence 465, Appl
7	107.2	22.0	854	16	US-10-345-887-465	Sequence 465, Appl	Sequence 465, Appl
8	107.2	22.0	854	16	US-10-641-643-1207	Sequence 1207, A	Sequence 1207, A
9	107.2	22.0	967	15	US-10-210-120-75	Sequence 75, Appl	Sequence 75, Appl
10	107.2	22.0	1076	9	US-09-925-300-70	Sequence 70, Appl	Sequence 70, Appl
11	101.4	20.8	375	9	US-09-740-563-1	Sequence 1, Appl	Sequence 1, Appl
12	101.4	20.8	375	15	US-10-255-576-1	Sequence 1, Appl	Sequence 1, Appl





PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM 000300  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-465

Query Match 22.0%; Score 107.2; DB 15; Length 854;  
Best Local Similarity 55.3%; Pred. No. 2.1e-23;  
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TCGTGTGTCCTTCCTCCCTCGTGGTCTCTGGTCAACCGGAACTGGTTAGTTTGGGG 134  
Db 155 TGGCAGTATCATGATCTTTGGCTACTGCGGCCCATGGGATTTGGTGAATTTCCACA 214  
QY 135 TGATGATCGAGAGATGACAGCAAG---TCCGCCCTGAGTACAAAGCATATGGCTGTT 191  
Db 215 GAATGATCAAGTTGACGACAGGAAGAACCCCACTCAGTTTATGGCTTCTACGGGTGCC 274  
QY 192 ACTGCGGCATCGTGGCTCCCTGCTGAGAGAGCTGGGCTGTGAGCCCAAACTGGAAAATATC 311  
Db 275 ACTGTGGCGTGGTGGCAGAGGATCCCCCAAGGATGCAACGATCGTGTCTGCTGCTC 334  
QY 252 AGACTGCTCTACGGGCTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAATATC 311  
Db 335 ATGACTGTTGCTACAACTCTGGAGAACTGGGATGTGGCACCACAAATTTCTGAGCTACA 394  
QY 312 TTTTCTCTGTGACGGAACGTGGCATTTCTGCGCCGGCAGGACCACTGCCAGCGGCTGA 371  
Db 395 AGTTTAGCAACTCGGGGACAGAACTCACTGTGCAAAACAGGACTCCTGCAGAGTCAAC 454  
QY 372 CTGCGAGTGTGACAGAGGGCTGCGCTCTGCTTTCGCGCGCAACCTGGGCACCTACAACC 431  
Db 455 TGTGTGAGTGTGATAGGCTGTGCGCACCTGTTTGTAGAAAACAGACGACTACAATA 514  
QY 432 GCAAAATATGCCATATCCCAACAGCTGTGACCGGGCCCAACCCCGCTGCTGA 487  
Db 515 AAAAGTACCAGTACTATTCCAATAAACTGTCAGAGGGAGCACCCCTCGTTGCTGA 570

RESULT 7  
US-10-342-887-465  
; Sequence 465, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 465  
; LENGTH: 854  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-465

Query Match 22.0%; Score 107.2; DB 16; Length 854;  
Best Local Similarity 55.3%; Pred. No. 2.1e-23;  
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TCGTGTGTCCTTCCTCCCTCGTGGTCTCTGGTCAACCGGAACTGGTTAGTTTGGGG 134

Db 155 TGGCAGTATCATGATCTTTGGCTACTGCGGCCCATGGGATTTGGTGAATTTCCACA 214  
QY 135 TGATGATCGAGAGATGACAGCAAG---TCCGCCCTGAGTACAAAGCATATGGCTGTT 191  
Db 215 GAATGATCAAGTTGACGACAGGAAGAACCCCACTCAGTTTATGGCTTCTACGGGTGCC 274  
QY 192 ACTGCGGCATCGTGGCTCCCTGCTGAGAGAGCTGGGCTGTGAGCCCAAACTGGAAAATATC 311  
Db 275 ACTGTGGCGTGGTGGCAGAGGATCCCCCAAGGATGCAACGATCGTGTCTGCTGCTC 334  
QY 252 AGACTGCTCTACGGGCTCTGGAGAGCTGGGCTGTGAGCCCAAACTGGAAAATATC 311  
Db 335 ATGACTGTTGCTACAACTCTGGAGAACTGGGATGTGGCACCACAAATTTCTGAGCTACA 394  
QY 312 TTTTCTCTGTGACGGAACGTGGCATTTCTGCGCCGGCAGGACCACTGCCAGCGGCTGA 371  
Db 395 AGTTTAGCAACTCGGGGACAGAACTCACTGTGCAAAACAGGACTCCTGCAGAGTCAAC 454  
QY 372 CTGCGAGTGTGACAGAGGGCTGCGCTCTGCTTTCGCGCGCAACCTGGGCACCTACAACC 431  
Db 455 TGTGTGAGTGTGATAGGCTGTGCGCACCTGTTTGTAGAAAACAGACGACTACAATA 514  
QY 432 GCAAAATATGCCATATCCCAACAGCTGTGACCGGGCCCAACCCCGCTGCTGA 487  
Db 515 AAAAGTACCAGTACTATTCCAATAAACTGTCAGAGGGAGCACCCCTCGTTGCTGA 570

## RESULT 8

US-10-641-643-1207  
; Sequence 1207, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

Jeffrey J. Seilhamer

Susan G. Stuart

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/641,643

FILING DATE: 14-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1207:

SEQUENCE CHARACTERISTICS:

LENGTH: 854 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK



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; CLONE: g19088
; SEQUENCE DESCRIPTION: SEQ ID NO: 1207 :
US-10-641-643-1207

Query Match      22.0%; Score 107.2; DB 16; Length 854;
Best Local Similarity 55.3%; Pred. No. 2.1e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTGGTGTCTCTTTGGCTCTCTGGTGGCTCTGTCTACCGGAACCTGGTTCAGTTTGGGG 134
DB 155 TGGCAGTGATCATGATCTTTGGCTCTCTGGCAGGCCATGGGAATTTGGTGAATTTCCACA 214

QY 135 TGATGATCGAAGATCAGCAGGCAAG--TCCGCCCTGCGAGTACCAAGACTATGGGTGTT 191
DB 215 GAATGATCAAGTTGACACAGGAAGAAAGCGGCACTCAGTTATGGTCTTACGGCTGCC 274

QY 192 ACTCGGCATCGGTGGTCCCACTGGCCGGTGGACCAAGACTGAGTGTGTGCCAGCC 251
DB 275 ACTGGCGTGGTGGCAGAGGATCCCAAGGATGCAACGGATCGCTGTGTCTCACTC 334

QY 252 ACGACTGCTGCTACGGGCTCTGAGAGCTGGCCCTCTGCTGTGAGCCCAACTGGAAGTATC 311
DB 335 ATGACTGTGCTACAAACGCTGAGAAACGTGGATGTGGCACCACCAATTTCTGAGCTACA 394

QY 312 TTTTCTCTGTGAGCAAGCTGGCAATTTTCTGCGCGGCGAGGACCACTGCCAGCGGTGA 371
DB 395 AGTTAGCAACTCGGGAGCAGATCACCCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 454

QY 372 CTTGCGAGTGTGCAAGAGGCTGCCCTCTGCTTTTCGCGCGGCGAGGACCACTGCCAGCGGTGA 431
DB 455 TGTGTGAGTGTGATAAGGCTCTGCCACCTGTTTGTGCTAGAAACAGACGACCTACAATA 514

QY 432 GCAATATGCCCATTTATCCCAACAGCTGTGACCGGGCCCACTGCCCGCTGTGTA 487
DB 515 AAAAGTACCAGTACTATTCOAATAAAGTGTGCTGAGGAGGAGCACCCTCTGTGCTGA 570

RESULT 9
US-10-210-120-75
; Sequence 75, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-75
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Query Match      22.0%; Score 107.2; DB 15; Length 967;
Best Local Similarity 55.3%; Pred. No. 2.2e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTGGTGTCTCTTTGGCTCTCTGGTGGCTCTGGTCAACCGGAACTGGTTCAGTTTGGGG 134
DB 292 TGGCAGTATCATGATCTTTGGCTCTCTGAGGCCCATGGGAATTTGGTGAATTTCCACA 351

QY 135 TGATGATCGAAGATGACAGGCAAG---TCCGCCCTGCGAGTACCAAGCACTATGGCTGTT 191
DB 352 GAATGATCAAGTTGACGAGGAAGGAGCGGCACTCAGTTATGGCTTCTACGGCTGCC 411
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QY 192 ACTGGCGCATCGGTGGCTCCCACTGGCCGGTGGACCAAGACTGACTGACTGTGCCACGCC 251
DB 412 ACTGTGGCGTGGTGGCAGAGATCCCCCAAGAGATGCAACGGATCGCTGTGTGCTCACTC 471

QY 252 ACGACTGTCTGTACGGGCGTCTGGAGAACTGGGCTGTGAGCCCAAACTGGAAAAGTATC 311
DB 472 ATGACTGTGTCTACAAACGCTCTGGAGAAACGTGGATGTGGCAACCAATTTCTGAGCTACA 531

QY 312 TTTTCTCTGTACGCAACGTGGCATTTTCTGCGCGGCGAGGACCACTGCCAGCGGTGA 371
DB 532 AGTTTAGCAACTCGGGAGCAGAATCACCCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 591

QY 372 CTTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTTCGCGCGCAACCTGGGCACTTACAACC 431
DB 592 TGTGTGAGTGTGATAAGGCTGTGCCACCTGTTTGTGTAGAAACAAAGACGACCTACAATA 651

QY 432 GCAATATGCCCATTTATCCCAACAGCTGTGACCGGGCCCACTGCCCGCTGTGTA 487
DB 652 AAAAGTACCAGTACTATTTCCAAATAAAGTGTGAGGAGGAGCACCCTCTGTGCTGA 707

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70
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Query Match      22.0%; Score 107.2; DB 9; Length 1076;
Best Local Similarity 55.3%; Pred. No. 2.3e-23;
Matches 230; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 75 TGTGGTGTCTCTTTGGCTCTCTGGTGGCTCTGGTCAACCGGAACTGGTTCAGTTTGGGG 134
DB 215 TGGCAGTGATCATGATCTTTGGCTCTCTGAGGCCCATGGGAATTTGGTGAATTTCCACA 274

QY 135 TGATGATCGAAGATGACAGGCAAG---TCCGCCCTGCGAGTACACAGCACTATGGCTGT 191
DB 275 GAATGATCAAGTTGACGAGGAAGAAAGCGGCACTCAGTTATGGCTTCTACGGCTGCC 334

QY 192 ACTGGCGCATCGGTGGCTCCCACTGGCCGGTGGACCAAGACTGACTGGTGTCTGCCAGCCC 251
DB 335 ACTGTGGCGTGGTGGCAGAGGATCCCCCAAGATGCAACGGATCGCTGTGTCACTC 394

QY 252 ACGACTGTCTACGGGCGTCTGGAGAACTGGGCTGTGAGCCCAAACTGGAAAAGTATC 311
DB 395 ATGACTGTGTCTACAAACGCTCTGGAGAAACGTGGATGTGGCACCACCAATTTCTGAGCTACA 454

QY 312 TTTTCTCTGTACGCAACGTGGCATTTTCTGCGCGGCGAGGACCACTGCCAGCGGTGA 371
DB 455 AGTTTAGCAACTCGGGAGCAGGAATCACCCTGTGCAAAACAGGACTCCTGCGAAGTCAAC 514

QY 372 CTTGCGAGTGTGAAAGAGGGCTGCCCTCTGTGTTTTCGCGCAACCTGGGCACTTACAACC 431
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Db 515 TGTGTGAGTGTGATAAGGCTGTGCGACCTGTTTGTAGAAACAAGACGACCTACAATA 574  
QY 432 GCAATATGCCATATATCCACAAGCTGTGACCGGGCCACCCCGCCTGCTGA 487  
Db 575 AAAAGTACCAGTACTATTCCATTAACACTGCAGAGGAGCACCCCTGTGCTGA 630

## RESULT 11

US-09-740-569-1  
; Sequence 1, Application US/09740569  
; Publication No. US2002017268A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Jerrold  
; APPLICANT: Elsbach, Peter  
; APPLICANT: Liang, Ning-Sheng  
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE  
; FILE REFERENCE: 5986/1B917US1  
; CURRENT APPLICATION NUMBER: US/09/740,569  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/172,467  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-740-569-1

Query Match 20.8%; Score 101.4; DB 9; Length 375;  
Best Local Similarity 56.3%; Pred. No. 1.2e-21;  
Matches 211; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 116 AACCTGGTTCAGTTTGGGTGATGATCGGACATCGGTGCTCCACTGCGCGGTGACCCAGT 172  
Db 1 AATTTGGTGAATTTCCACAGCTGATCAAGTTGACGACGAGAAAGGACCGCACTCAGT 60  
QY 173 TACAAGCACTATGGCTGTACTCGGCATCGGTGCTCCACTGCGCGGTGACCCAGT 232  
Db 61 TATGGCTTCTACGGCTGCCACTGTGGCGTGGGACGAGATGCCCAAGATGCAACG 120  
QY 233 GACTGTGCTGCCACGCCACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGCTGTGAG 292  
Db 121 GATCGCTGTGTGCTCACTCATGCTGTTGCTACAAACGCTGGAGAAACGTTGGATGTGC 180  
QY 293 CCCAACTGGAAAAGTATCTTTCTCTGTCACGCAACGTGGCATTTTCTGCGCGCGGAGG 352  
Db 181 ACCAAATTTCTGAGTACAAAGTTTAGCACTCGAAGACGAGCAATCACCTGTGCAAAACAG 240  
QY 353 ACCACCTGCAGCGGTGACCTCGGAGTGTGACAAAGAGGGTGCCTCTGCTTTCGCCGC 412  
Db 241 GACTCCTGCAGAGTCAACTGTGTGAGTGTGATAGGCTGTGCGCACCTGTTTGTCTAGA 300  
QY 413 AACCTGGGCACTACACCGGAAATATGCCCATTTATCCCAACAGCTGTGCACCGGCC 472  
Db 301 AACAAAGAGACCTACAATAAAGTACCAGTACTATTCCATAAACAACACTGCAGAGGGAGC 360  
QY 473 ACCCGCGCTGTGA 487  
Db 361 ACCCTCGTTGTGA 375

## RESULT 12

US-10-255-576-1  
; Sequence 1, Application US/10255576  
; Publication No. US2003016182A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Jerrold  
; APPLICANT: Elsbach, Peter  
; APPLICANT: Liang, Ning-Sheng  
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE  
; FILE REFERENCE: 5986/1B917US1

; CURRENT APPLICATION NUMBER: US/10/255,576  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US/09/740,569  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/172,467  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-255-576-1

Query Match 20.8%; Score 101.4; DB 15; Length 375;  
Best Local Similarity 56.3%; Pred. No. 1.2e-21;  
Matches 211; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 116 AACCTGGTTCAGTTTGGGTGATGATCGGACATCGGTGCTCCACTGCGCGGTGACCCAGT 172  
Db 1 AATTTGGTGAATTTCCACAGCTGATCAAGTTGACGACGAGAAAGGACCGCACTCAGT 60  
QY 173 TACAAGCACTATGGCTGTACTCGGCATCGGTGCTCCACTGCGCGGTGACCCAGT 232  
Db 61 TATGGCTTCTACGGCTGCCACTGTGGCGTGGGACGAGATGCCCAAGATGCAACG 120  
QY 233 GACTGTGCTGCCACGCCACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGCTGTGAG 292  
Db 121 GATCGCTGTGTGCTCACTCATGCTGTTGCTACAAACGCTGGAGAAACGTTGGATGTGC 180  
QY 293 CCCAACTGGAAAAGTATCTTTCTCTGTCAGGCAACGTGGCATTTTCTGCGCGCGGAGG 352  
Db 181 ACCAAATTTCTGAGTACAAAGTTTAGCACTCGAAGACGAGCAATCACCTGTGCAAAACAG 240  
QY 353 ACCACCTGCAGCGGTGACCTCGGAGTGTGACAAAGAGGGTGCCTCTGCTTTCGCCGC 412  
Db 241 GACTCCTGCAGAGTCAACTGTGTGAGTGTGATAGGCTGTGCGCACCTGTTTGTCTAGA 300  
QY 413 AACCTGGGCACTACACCGGAAATATGCCCATTTATCCCAACAGCTGTGCACCGGCC 472  
Db 301 AACAAAGAGACCTACAATAAAGTACCAGTACTATTCCATAAACAACACTGCAGAGGGAGC 360  
QY 473 ACCCGCGCTGTGA 487  
Db 361 ACCCTCGTTGTGA 375

## RESULT 13

US-10-016-149-3  
; Sequence 3, Application US/10016149  
; Publication No. US20030100524A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP V (CA2+-  
; TITLE OF INVENTION: DEFENDENT) EXPRESSION  
; FILE REFERENCE: RTS-0325  
; CURRENT APPLICATION NUMBER: US/10/016,149  
; CURRENT FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 84  
; SEQ ID NO 3  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (133)...(549)  
US-10-016-149-3

Query Match 20.5%; Score 99.8; DB 15; Length 1016;  
Best Local Similarity 54.5%; Pred. No. 4.8e-21;  
Matches 222; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

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QY 82 GTTCTTTGCCCTCTGTTGGCTGTGTCACCGGAACTCGTTTCAGTTTGGGGTGATGAT 141
Db 159 GTTCTGCTGTAGTGTGCTGTGTCAGAGGAGGCTTGTGCACTAAATCAATGAT 218
QY 142 CGAGAAGATGACAGCAAGTCGCCCTG---CAGTACAAAGACTATGCTGTACTGCGG 198
Db 219 CGAGAAGGTGACAGGAAGAACGCCCTGACAACTACGGCTTCTACGGCTGTACTGCGG 278
QY 199 CATGGTGGCTCCCACTGGCCGGTGGACCACTGACTGTGTCGCCACGCCCACTG 258
Db 279 CTGGGGGGCGAGAAACCCCAAGGATGGCAGATTGGTGTGTTGGGGCGCATGACCA 338
QY 259 CTGCTACGGGGCTGTGGAAGAGCTGGCTGTGAGCCCAAACTGAAAAAGTATCTTTTCTC 318
Db 339 CTGCTATGGCGGCTGGAGGAAGAGGCTGCAACATTGCGACACAGTCTTACAAATACAG 398
QY 319 TGTACGAAACGTGGCATTTTCTGGCGGGGAGACACACCTGCGAGCGGTGACTCGGA 378
Db 399 ATTGCGTGGGGCGTGGTCACTCGAGCCCGGCCCTTCTGCCATGTGAACCTCTGTGC 458
QY 379 CATGGTGGCTCCCACTGGCCGGTGGACCACTGACTGTGTCGCCACGCCCACTG 258
Db 279 CTGGGGGGCGAGAAACCCCAAGGATGGCAGATTGGTGTGTTGGGGCGCATGACCA 338
QY 259 CTGCTACGGGGCTGTGGAAGAGCTGGCTGTGAGCCCAAACTGAAAAAGTATCTTTTCTC 318
Db 339 CTGCTATGGCGGCTGGAGGAAGAGGCTGCAACATTGCGACACAGTCTTACAAATACAG 398
QY 319 TGTACGAAACGTGGCATTTTCTGGCGGGGAGACACACCTGCGAGCGGTGACTCGGA 378
Db 399 ATTGCGTGGGGCGTGGTCACTCGAGCCCGGCCCTTCTGCCATGTGAACCTCTGTGC 458
QY 379 GTGTGACAAGAGGCTGCGCTCTGTTTCGCGCGCAACTGGGCACTTACAAACGCAATA 438
Db 459 CTGTGACCGGAAGCTGCTCTACTGCTCAAGAGAAACCTACGAGCTACAAACCCAGTA 518
QY 439 TGCCCATATCCCAACAGCTGTGACCGGGCCCAACCGCCCGCTGCT 485
Db 519 CCAATACTTCCCAACATCTCTGCTCTAGGCGCTCCCGAGGAGCT 565
RESULT 14
US-10-647-426-17
; Sequence 17, Application US/10647426
; Publication No. US20040110197A1
; GENERAL INFORMATION:
; APPLICANT: Patton, Jodi L.
; APPLICANT: Skinner, Michael X.
; TITLE OF INVENTION: A METHOD OF DETERMINING TUMOR CHARACTERISTICS BY
; DETERMINING ABNORMAL COPY NUMBER OR EXPRESSION LEVEL OF
; TITLE OF INVENTION: LIPID-ASSOCIATED GENES
; FILE REFERENCE: PATRICK EAGLEMAN: EMBOL-X 252/124
; CURRENT APPLICATION NUMBER: US/10/647,426
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/576,052
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1016)
; OTHER INFORMATION: The sequence of the cDNA coding for Phospholipase
; OTHER INFORMATION: A2
US-10-647-426-17
Query Match 20.5%; Score 99.8; DB 17; Length 1016;
Best Local Similarity 54.5%; Pred. No. 4.8e-21;
Matches 222; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
QY 82 GTTCTTTGCCCTCTGTTGGCTGTGTCACCGGAACTCGTTTCAGTTTGGGGTGATGAT 141
Db 159 GTTCTGCTGTAGTGTGCTGTGTCAGAGGAGGCTTGTGCACTAAATCAATGAT 218
QY 142 CGAGAAGATGACAGCAAGTCGCCCTG---CAGTACAAAGACTATGCTGTACTGCGG 198
Db 219 CGAGAAGGTGACAGGAAGAACGCCCTGACAACTACGGCTTCTACGGCTGTACTGCGG 278
QY 199 CATGGTGGCTCCCACTGGCCGGTGGACCACTGACTGTGTCGCCACGCCCACTG 258
Db 279 CTGGGGGGCGAGAAACCCCAAGGATGGCAGATTGGTGTGTTGGGGCGCATGACCA 338
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QY 259 CTGCTACGGGGCTCTGGAAGAGCTGGGCTGTGAGCCCAAACTGGAAGTATCTTTTCTC 318
Db 339 CTGCTATGGCGGCTGGAGGAAGAGGCTGCAACATTGCGACACAGTCTCAAAATACAG 398
QY 319 TGTACGAAACGTGGCATTTTCTGGCGGGGAGACACACCTGCGAGCGGTGACTCGGA 378
Db 399 ATTGCGTGGGGCGTGGTCACTCGAGCCCGGCCCTTCTGCCATGTGAACCTCTGTGC 458
QY 379 GTGTGACAAGAGGCTGCGCTCTGTTTCGCGCGCAACCTGGGCACCTACAAACGCAATA 438
Db 459 CTGTGACCGGAAGCTGCTCTACTGCTCAAGAGAAACCTACGAGCTACAAACCCAGTA 518
QY 439 TGCCCATATCCCAACAGCTGTGACCGGGCCCAACCGCCCGCTGCT 485
Db 519 CCAATACTTCCCAACATCTCTGCTCTAGGCGCTCCCGAGGAGCT 565
RESULT 15
US-10-198-846-10988
; Sequence 10988, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongsao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10988
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1064..1065, 1066, 1067, 1068
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-10988
Query Match 20.4%; Score 99.4; DB 14; Length 1068;
Best Local Similarity 55.6%; Pred. No. 6.5e-21;
Matches 232; Conservative 0; Mismatches 181; Indels 4; Gaps 2;
QY 75 TGCTGGTGTCTCTTTCCTTTCCTGCTGTGCTGTGTCACCGGGAACCTGGTTTCAGTTTGGG 134
Db 244 TGGCAGTGATCATGATCTTTGGCTTACTGAGGCCCATGGAAATTTGGTGAATTTCCACA 303
QY 135 TGATGATCGAGAAGATGACAGGCAAG---TCGCGCTTCAGTACACAGTACTATGGTGT 191
Db 304 GAATGATCAAGTTGACGACAGGAAGAAAGCCGCACTCAGTTTATGCTTCTACGGCTGCC 363
QY 192 ACTGCGGCATCGGTGGCTCCACTGCGGTGACAGCACTGACTGCTGCTGCCAGCCC 251
Db 364 ACTGCGCGTGGGTGGCAGAGGATCCCCAAGGATGCAACGGGATCTGCTGTGTCACTC 423
QY 252 ACCACTGCTCTCTACGGGCGTCTCGAAGAGTGGGCTGTGAGCCCAAACTGGAAGATATC 311
Db 424 ATGACTGTGCTACAAACGCTCTGAGAAAGGTGATGTGGCACCATAATTTCTGAGCTACA 483
QY 312 TTTTCTCTGTACGGAACGTGGCATTTTTCGCGCGGAGGACCACTGCGCAGGGCTGA 371
Db 484 AGTTTAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTTCAGAAAGTCAAC 543
QY 372 CCTGCGAGTGTACAGAGGGCTGCGCTCTGCTTTTGC -CGCAACTGGGCACCTCAAC 430
Db 544 TGTGTAGTGTGATAGGCTGTGCCACCTGTTTGTCTAGAAACAGAGACCTACAAT 603
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**Qy**      CGAAATATGCCCATTTATCCCAACAAGCTGTGACGGGGCCCACC GCCCGCCTGTA 487  
         | | | | |  
**Dd**      AAAAAGTACCAGTACTATTTC AATAAAC TGCAGAGGGAGCACCCCC TGTTGCTGA 660  
         | | | | |

Search completed: November 13, 2004, 06:51:37  
Job time : 275 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 05:00:27 ; Search time 1627 Seconds  
(without alignments)  
10907.283 Million cell updates/sec

Title: US-10-088-092A-29  
Perfect score: 487  
Sequence: 1 ctgcttctctctgcctt.....ggccaccacccgcctgctga 487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.4	95.2	465	AY417606	Homo sapi
2	308.8	63.4	464	AY417607	AY417607 Pan trogl
3	308.6	63.4	462	AY417608	AY417608 Mus muscu
4	308.6	63.4	537	BX519916	BX519916 BX519916
5	308.6	63.4	728	BY741324	BY741324 BY741324
6	307.8	63.2	726	CB597840	CB597840 AGENCOURT
7	305.6	62.8	480	BE133458	BE133458 UG33408.Y
8	260.6	53.5	381	BE128774	BE128774 DEPA254
9	217.4	44.6	436	2 BB851133	BB851133 BB851133
10	190.4	39.1	320	AF046275	AF046275 AF046275
11	188.2	38.6	309	CG473029	CG473029 OST327 Mu
12	180.2	37.0	342	BY010605	BY010605 BY010605
13	147.6	30.3	701	CF249871	CF249871 esa005.e0
14	139.2	28.6	544	2 BB753895	BB753895 BB753895
15	134	27.5	520	6 CD734010	CD734010 4047352.1
16	133.4	27.4	368	5 BY014871	BY014871 BY014871
17	131	26.9	466	2 BE136551	BE136551 UG33408.X
18	132	25.1	625	5 BQ781867	BQ781867 UI-R-FFO-
19	115.2	23.7	549	8 BH358238	BH358238 CH230-107
20	113.8	23.4	465	2 BB819195	BB819195 BB819195
21	110.4	22.7	713	8 AZ661866	AZ661866 LM0540U17
22	109.2	22.4	820	5 EQ483760	EQ483760 UI-H-EUO-
23	109	22.4	417	5 BQ31930	BQ31930 UI-1-CFO-
24	108.8	22.3	605	4 BM695558	BM695558 UI-B-CQ1-

ALIGNMENTS

RESULT 1  
AY417606  
LOCUS Homo sapiens HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence, 465 bp DNA linear GSS 12-DEC-2003  
DEFINITION Homo sapiens HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY417606  
VERSION AY417606.1 GI:39773566  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 465)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 465)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source  
1..465  
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/db\_xref="taxon:9606"  
<1..>465  
/locus\_tag="HCM6280"

ORIGIN  
Query Match 95.2%; Score 463.4; DB 9; Length 465;  
Best Local Similarity 99.8%; Pred. No. 7.5e-111;  
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 23 ATGCTCTTGTGACCTCCCTCCCGCAACCTGGGATGAATCTCCCGACGCTGCTGGT 82  
DB 1 ATGCTCTTGTGACCTCCCTCCCGCAACCTGGGATGAATCTCCCGACGCTGCTGGT 60





Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E.E., Dragani, T.A.,  
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Glasi, C., Godik, A., Gough, J., Grimmond, S.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konegaya, A.,  
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Numata, K., Okido, T., Favan, W.J., Perte, G., Pesole, G.,  
Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222

/clone="G370044J20"  
 /cell\_type="B16 F10Y cells"  
 /clone\_lib="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN

Query Match 53.4%; Score 308.6; DB 6; Length 728;  
 Best Local Similarity 80.3%; Pred. No. 3.7e-70;  
 Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CTTCCCTTCCCGCAACCTGGGATGAATATCCCCACGTCGTGCTGTCCTTGCCTCCT 96  
 Db 160 CCCCCTGCCTACCTCCCCAGGATGAACCTCCCAATTGCCCTGGCTGCCTTTGCCCTCCT 219  
 QY 97 GGTGGCTCTGCTCACCGGAACTGTTCACTTTGGGTTGATGTCGAGAAGATGCAGG 156  
 Db 220 GGTGCCCTTGGCTGGCGGGAACCTGTCAGTTTGAGTGTGATGATGAGAGAATGACGGG 279  
 QY 157 CAAGTCGGCCTGCAGTCAACACGACTATGGCTGTTACTGGGGCATCGTGCGCTCCCACTG 216  
 Db 280 AAGCCTGCCCCTGCAGTCAATGACTATGGCTGCTATTGGCGTGCCTGGCTCCCACTG 339  
 QY 217 GCGGTGGACGACGACTGCTGTGCTGCCACGCCACGAGCTGCTGTACGGGCGTCTGGA 276  
 Db 340 GCCAGTGGACGACGAGGATGTTGTTGTATGATGCCCATGACTGCTGTATGGCCGCTGGA 399  
 QY 277 GAAGCTGGGCTGTGAGCCCAACTGGAAGATATCTTTCTCTGTGACGAACTGGCAT 336  
 Db 400 GAAGCTGGGCTGTGACCCCAAGCTGGAAAGTACCTCTTCTCTATCACTCGACACACAT 459  
 QY 337 TTCTCGCCGCGGACGACCACTGCCAGCGGTGACCTCGGAGTGTGACAAAGGCGTGC 396  
 Db 460 CTCTCTGCTGTAGAACGGCTTGCCAGCGGCATACCTGCGAGTGTGACAAAGAGAGCTGC 519  
 QY 397 CTTCTGCTTTGCGCGCAACTGGGCACTTACACGCCAAATATGCCCATATCCCAACAA 456  
 Db 520 TCTTTGCTTTGCGCAACTGAACTTACACCGCAAGATGCCCACATACCCCAACAA 579  
 QY 457 GCTGTGCACGGGCGCCACCGCCGCTGTA 487  
 Db 580 GCTGTGTAAGGGCCACCCACCCCTGCTGA 610

RESULT 6  
 CB597840  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CB597840 726 bp mRNA linear EST 03-APR-2003  
 AGENCOURT 12972149 NIH MGC 178 Mus musculus cDNA clone  
 IMAGE:30237098 5', mRNA sequence.  
 CB597840  
 CB597840.1 GI:29515696  
 EST.  
 Mus musculus  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 726)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps@mail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Michael Brownstein Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDCM57 row: h column: 03  
 High quality sequence stop: 557.  
 Location/Qualifiers  
 1. .726  
 /organism="Mus musculus"  
 /mol\_type="mRNA"

FEATURES  
 source

## FEATURES





Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 381)  
 Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,  
 McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.  
 Expressed sequence tags of cDNA clones from rat dermal papilla  
 cells

Unpublished (2000)

Contact: Sleeman MA

Biology

Genesis Research and Development Corporation Limited

P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand

Tel: 0064 9 373 5600

Fax: 0064 9 373 2189

Email: m.sleeman@genesis.co.nz

Seq primer: T3 forward

High quality sequence stop: 381.

FEATURES  
 source

1..381

Location/Qualifiers

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Dark-Agouti"

/db\_xref="taxon:10116"

/tissue\_type="vibrissae"

/cell\_type="dermal papilla"

/clone\_lib="Rat Lambda ZAP Express Library"

ORIGIN

Query Match 53.5%; Score 260.6; DB 2; Length 381;  
 Best Local Similarity 83.4%; Pred. No. 1.3e-57;  
 Matches 296; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 98 GTGGCTCTGGTACACCGGACCTGGTTCAGTTGGGTCATCATCAGAGATGACAGC 157

Db 27 GCGCCCTGGCTGGTGGGACCTGGTCCAGTTGGAGTAATGATTGAGAGATGACAGGA 86

QY 158 AAGTCGCGCTGAGTACACGACACTATGCTGTACTCGGCGATCGGTGCTCCACTGG 217

Db 87 AAGCCGCGCTGAGTACACGACACTATGCTGTACTCGGTGCTCCACTGG 146

QY 218 CCGTGGACAGACTGACTGTGCTGCCAGCCAGACTGTGCTAGCGGCTGTGGAG 277

Db 147 CCGTGGACAGAGGATGCTGCTGTACGCGCCATGACTGTGCTATGCGCGCTGGAG 206

QY 278 AAGCTGGCTGTGAGCCCAAACTGGAAGATATCTTTCTCTGTCAGCGAAGCTGGCAT 337

Db 207 AAGCTGGCTGTGATCCCAACTGGAAGATATCTTTCTCTATCACCAGGACACATC 266

QY 338 TTCTGCGCGGAGGACACCTGCGAGCGCTGACCTGAGTGTGACAAGAGGCTGCC 397

Db 267 TTCTGCTGTGTAGAACGACTTGCAGCGGACAGCTGTGAGTGTGACAAGAGAGCTGCC 326

QY 398 CTCTGCTTTTCGCGCAACCTGGGCACTACACCGCAATATGCCATTATCCCA 452

Db 327 CTCTGCTTTTCGCAACCTGGGCACTTATACCGCAATATGCTCACTACCCCA 381

RESULT 9

BB851133

LOCUS

BB851133 436 bp mRNA linear EST 26-NOV-2001

DEFINITION

Clone G270014B19 5', mRNA sequence.

ACCESSION

BB851133

VERSION

BB851133.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1. (bases 1 to 436)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hirokawa, T., Hirozane, T., Imotani, K.,

Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,  
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,  
 Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Tanaka, T., Tomaru, A., Toya, I., Watanishi, A., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.  
 2001)

Unpublished (2001)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E.,

Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

FEATURES

source

1..436

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="G270014B19"

/cell\_type="melanocyte"

/clone\_lib="RIKEN full-length enriched, melanocyte"

ORIGIN

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Best Local Similarity 73.4%; Pred. No. 3e-46;

Matches 278; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 37 CCTCCCTTCCCGCAACCTGGGATGAATCTCCACGCTGCTGCTTCTTCTTCTCTCT 96

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QY 97 GGTGGCTCTGGTCAACCGGAACTGGTTTCAGTTTGGGTGATCATCAGAGATGACAG 156

Db 107 GGTGGCTCTGGTGGGGGAACTGGTTCAGTTTGGAGTGAATGAGAGATGACGG 166

QY 157 CAAGTCGGCTGCACTGACAGACTATGCTGTCTACTCGGCACTGCTGGCTCCACTG 216

Db 167 AAAGCTGCTGCTGCACTGACATGCTATGCTGTCTATGGGCTGCTGGCTCCACTG 226

QY 217 GCGGTGGACCACTGCTGCTGCTGCCACCGCACTGCTGCTACGGCGCTGGA 276

Db 227 GCAGTGGACGAGACGAGTGTGTCTATGCCATGACTGCTGTATGGCGCTGGA 286

QY 277 GAAGCTGGCTGTGAGCCCAAACTGGAAGATATCTTTCTCTGTGAGCAAGCTGGCAT 336

Db 287 GAAGCTGGCTGTGAGCCCAAGCTGGAAGATACCTCTTCTCTATCACTCGAGAAACAT 346

QY 337 TTCTCTGGCGGCGAGGACCACTGCCAGGCTGACCTCGAGTGTGACAAGAGGCTGC 396

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Db 347 CTTCTGTGCTGTAGAAAGCGGTTCACCGGATACCTGCCAGCTGTGACAAAGAGCCG 406
QY 397 CCTCTGCTTTGGCCGCAAC 415
Db 407 ATCTGCTTTGCCAAACC 425

RESULT 10
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LOCUS AF046275 Mus musculus 129Sv/Ev Mus musculus genomic clone OST327,
DEFINITION genomic survey sequence.
ACCESSION AF046275
VERSION AF046275.1 GI:3005146
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 320)
Zambrowicz,B.P., Friedlich,G.A., Buxton,B.C., Lilleberg,S.L.,
Person,C. and Sands,A.T.
Disruption and sequence identification of 2,000 genes in mouse
embryonic stem cells
JOURNAL Nature 392 (6676), 608-611 (1998)
MEDLINE 98219085
PUBMED 9560157
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
OmniBank Sequence Tag
Class: exon-trapped.
Location/Qualifiers
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Best Local Similarity 78.5%; Pred. No. 3.6e-39;
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 146 AAGATGACAGGCAAGTCCGCCCTGCAGTACACGACTATGGTGTACTGCGGCATCGGT 205
Db 5 AAGAGANGAGGAAACCTGCCCTGNAGTACATNACTATGGTGTATTCGCGTTCGGT 64
QY 206 GGTCTCCACTGCGCGT-GGACCAGACTGCTGCTGCCAGCCGACGACTGCTGCTA 264
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QY 265 CGGGCTCTGGAGAACTGGCGTGTGAGCCCAAACTGGAAAAGTATCTTTCTGTCTG 324
Db 125 TGCGCGCTGGAGAACTGGCGTGTGACCCCAAGCTGGAAAAGTACTCTTCTCTATCA 184
QY 325 CGAACTGGGATTTCTGCGCGGAGGACCACTCCAGCGGCTGACCTGGAGTGCA 384
Db 185 TCGAGACAAACATCTTCTGTGTGTTAAACGGGTTCGCAGCGGCATACCTGCGAATGTA 244
QY 385 CAAGAGGGCTGCCCTCTGCTTCGCGCAACTGGGCAGCTACAAACGCAATATGCCCA 444
Db 245 CAA-AAAACCGCTCTGCTTTTCGCCACACCTGAACCTTACACCGCAANTATGCCCA 303
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## RESULT 11

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LOCUS CG473029 Mus musculus 129Sv/Ev Mus musculus genomic clone OST327,
DEFINITION genomic survey sequence.
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ACCESSION CG473029
VERSION CG473029.1 GI:37223742
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KEYWORDS Mus musculus (house mouse)
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SOURCE Mus musculus
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## ORGANISM

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

## REFERENCE

## AUTHORS

```
1 (bases 1 to 309)
Zambrowicz,B.P., Abulin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,F., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
```

Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

## JOURNAL

## COMMENT

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

## FEATURES

## source

1..309

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST327"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

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Best Local Similarity 79.3%; Pred. No. 1.3e-38;

Matches 245; Conservative 0; Mismatches 62; Indels 2; Gaps 2;

QY 154 AGGCAAGTCGCGCCTCGAGTACACGACTATGGTGTACTGGGCATCGGTGCTCCCA 213

Db 2 AGGGAACCTGCCCTGNAGTACATNACTATGGTGTATTCGCGTTCGGTTCGCTCCCA 61

QY 214 CTGCGCGGT-GGACCAGACTGACTGGTGTGCCACGCCACGACTGCTGTACGGCGTC 272

Db 62 CTGCGCCAGTGGAGCGAAACGGATTGGTGTTCATGCCCATGACTGCTGTATGGCGGCC 121

QY 273 TGGAGAGCTGGGTGTGAGCCCAACTGGAAAAGTATCTTTCTGTCAGCGAACGTG 332

Db 122 TGGAGAACTGGGTGTGACCCCAAGCTGGAAAAGTACCTCTTCTATCACTCGAGACA 181

QY 333 GCATTTTCTGCGCGCGGAGGACCACTGCCAGCGGCTGACCTGCGAGTGTGACAAGGG 392

Db 182 ACATCTTCTGCTGGTAAACGGCTTGCCAGCGGCATACCTGCGAATGTGACAA-AAAA 240

QY 393 CTGCGCTCTGTTTCGCGCGAACCTGGGCACCTACACCGCAATATGCCCATTCCTCA 452

Db 241 CCGCTCTCTGTTTCGCCACAACTGAACACTTACAAACCGCAANTATGCCCATTCACCCA 300

QY 453 ACAAGCTGT 461

Db 301 ACAAGCTGT 309

RESULT 12  
 BY010605  
 LOCUS  
 DEFINITION BY010605 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus  
 musculus CDNA clone G730021C18 5', mRNA sequence.  
 BY010605  
 ACCESSION BY010605.1 GI:26070854  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Mus musculus (house mouse)  
 REFERENCE  
 AUTHORS  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 342)  
 Okazaki, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomari, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,  
 Chotia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, I.A.,  
 Fietcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayashizaki, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, J.,  
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 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
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 cDNA, mRNA sequence.  
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 1 (bases 1 to 701)  
 Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J.,  
 Clausse, A.M. and Zoorob, R.  
 A collection of chicken ESTs from activated immune cells  
 Unpublished (2003)  
 Contact: Zoorob R  
 UPB 1983  
 CRRS  
 7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France  
 Tel: 33 1 49 58 35 00  
 Fax: 33 1 49 58 33 81  
 Email: zoorob@vif.cnrs.fr.  
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GenCore version 5.1.6  
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Run on: November 13, 2004, 03:57:42 ; Search time 1690 Seconds

(without alignments)  
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Title: US-10-088-092A-29

Perfect score: 487

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_dat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	476.4	97.8	478	9	BC069116 Homo sapi
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6	308.6	63.4	870	10	AF166098 Mus muscu
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8	308.6	63.4	883	6	BD013141 A gene en
9	308.6	63.4	883	10	AF112984 Mus muscu
10	190.4	39.1	320	6	E37217 Gene encodi
11	190.4	39.1	320	6	BD013128 A gene en
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13	144	29.6	157470	2	AL360079 Homo sapi
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15	115.2	23.7	282515	2	AC118094 Rattus no
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23	108.8	22.3	1160	6	CQ493657	CQ493657 Sequence
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25	108.8	22.3	1160	6	CQ497372	CQ497372 Sequence
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43	100	20.5	372	6	I09516	I09516 Sequence 6
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#### ALIGNMENTS

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DEFINITION	BD013155				
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SOURCE	Homo sapiens				
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REFERENCE	1 (bases 1 to 487)				
AUTHORS	Ishizaki, J., Suzuki, N. and Hanasaki, K.				
TITLE	A gene encoding novel human secretory type phospholipase A2				
JOURNAL	PATENT: WO 0121775-A 28 29-MAR-2001;				
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	PI JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI				
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Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 478)  
 Strausberg, R.  
 Direct Submission  
 Submitted (16-APR-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
 Tissue Procurement: Anup Madan, University of Iowa  
 cDNA Library Preparation: Anup Madan, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Neurogenomics Research Lab,  
 200 B EMRE, University of Iowa, Iowa City, IA-52242  
[anup-madan@uiowa.edu](mailto:anup-madan@uiowa.edu)  
 Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan

Clone distribution: MGC clone distribution information can be found  
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 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 TITLE Kits, such as nucleic acid arrays, comprising a majority of  
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 JOURNAL Patent: WO 02068579-A 13131 06-SEP-2002;  
 PE Corporation (NY) (US)  
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VERSION     1
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1 (bases 1 to 762)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kertman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 762)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Marcelo Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Luisa Prabu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacques
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 67 Row: K Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6755091.
Location/Qualifiers
1. .762
/organism="Mus musculus"
/mol_type="mRNA"

FEATURES
source
RESULT 5
LOCUS      BC027524
DEFINITION Mus musculus phospholipase A2, group IIE, mRNA (cdna clone
ACCESSION  BC027524
VERSION     1
KEYWORDS   MGC.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 762)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Ustin,T.B., Tohiyuki,S.,
Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kertman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 762)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Marcelo Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Luisa Prabu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacques
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 67 Row: K Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6755091.
Location/Qualifiers
1. .762
/organism="Mus musculus"
/mol_type="mRNA"

FEATURES
source

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AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.  
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes

J. Biol. Chem. 274 (44), 31195-31202 (1999)  
20002639

PUBMED 10531313

REFERENCE Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.  
TITLE Direct Submission  
JOURNAL Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France

## FEATURES

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## ORIGIN

Query Match 63.4%; Score 308.6; DB 10; Length 870;  
Best Local Similarity 80.3%; Pred. No. 3.6e-67;  
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CCTCCCTCCCGCAACCTGGAGTGAATCTCCCAAGTGTGCTGTCTCTTTGCTCT 96  
Db 140 CCCCCTGCTACTCCCGCAGAGTAACTCCCACTTGGCTTGGCTTTGCTCTCT 199  
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QY 337 TTTCTGCGCGCAGGACCACTCCAGCGCTGACCTGGAGTGTGACAGAGGGCTGC 396  
Db 440 CTTCTGTCTGTAGAACGGTTGCCAGCGCATACCTGGAGTGTGACAGAGAGCCGC 499  
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## RESULT 7

E37230

LOCUS

883 bp DNA linear

PAT 31-JAN-2002

## DEFINITION

Gene encoding novel mouse secretory phospholipase A2.

E37230

ACCESSION E37230.1 GI:18626640

VERSION JP 2000166568-A/14.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

REFERENCE

1 (bases 1 to 883)

Ishizaki, J., Suzuki, N. and Hanasaki, K.

AUTHORS

TITLE

Gene encoding novel mouse secretory phospholipase A2

JOURNAL Patent: JP 2000166568-A 14 20-JUN-2000;

SHIONOGI & CO LTD

COMMENT

OS Mus musculus (mouse)

PN JP 2000166568-A/14

PD 20-JUN-2000

PF 09-DEC-1998 JP 1998349604

PR JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI

PI PC C12N15/09, C07K16/40, C12N5/10, C12N9/16, C12Q1/44// (C12N15/09, PC

C12R1/91),

PC (C12N5/10, C12R1/91), (C12N9/16, C12R1/91), C12N15/00, C12N5/00, PC

(C12N15/00, C12R1/91), (C12N5/00, C12R1/91)

CC

Key Location/Qualifiers

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FT mat\_peptide (223)..(591).

Location/Qualifiers

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ORIGIN

Query Match 63.4%; Score 308.6; DB 6; Length 883;

Best Local Similarity 80.3%; Pred. No. 3.6e-67;

Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 37 CTTCCCTTCCCGCAACCTGGAGTGAATCTCCCAAGTGTGCTGTCTCTTTGCTCT 96

Db 144 CCCCCTGCTACTCCCGCAGGATGAACCTCCCATTTGCCCTGGCTTGGCTTGGCTCT 203

QY 97 GGTGGCTGTGTCACCGGAACTGTTTCAGTTTGGGGTGATGATCGAGAAGATGACAGG 156

Db 204 GGTGCCCTTGGCTGGCGGAACTGCTCCAGTTTGGAGTGTGATGAGAGATGACGGG 263

QY 157 CAAGTCGGCTCAGTACACGACTATGGCTGTCTTACTCGGCACTCGGTGGCTCCCACTG 216

Db 264 AAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323

QY 217 GCGGTGGACCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276

Db 324 GCGGTGGACCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383

QY 277 GAAGCTGGCTGTGAGCGCCCAACTGGAAGTATCTTTTCTCTGTCAGCGAACTGGCAT 336

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QY 337 TTTCTGCGCGCAGGACCACTGCGCGGCTGCTGCGAGTGTGACAGAGGGCTGC 396

Db 444 CTTCTGTGTGTAGAACGGTTGCCAGCGCATACCTGCGAGTGTGACAGAGGGCTGC 503

QY 397 CTTCTGCTTTCCCGCAACTGGGCACTTCAACCGCAAAATATGCCCAATTATCCCAACA 456

Db 504 TTTTGTCTTTCCCGCAACTGGAACCTTCAACCGCAAGTATGCCCACTATCCCAACA 563

QY 457 GCTGTGACCGGGCCACCCCGCTGTGA 487

Db 564 GCTGTGACTGGGGCCACCCACCTGTGA 594

## RESULT 8

BD013141

LOCUS BD013141 883 bp DNA linear PAT 02-AUG-2002  
DEFINITION A gene encoding novel human secretory type phospholipase A2.  
ACCESSION BD013141  
VERSION BD013141.1 GI:22093330  
KEYWORDS WO 0121775-A/14.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 883)  
AUTHORS Ishizaki, J., Suzuki, N. and Hanasaki, K.  
TITLE A gene encoding novel human secretory type phospholipase A2  
JOURNAL Patent: WO 0121775-A 14 29-MAR-2001;  
SHIONOGI & CO LTD, JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI  
COMMENT OS Mus musculus (mouse)  
PN WO 0121775-A/14  
PD 29-MAR-2001  
PF 18-SEP-2000 WO 2000JP006344  
PR 21-SEP-1999 JP 99P 266615  
PI JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI  
PC C12N9/20, C12N15/55, C12P21/02, C12P21/08, C07K16/40 CC  
PH Key Location/Qualifiers  
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FT mat\_peptide (223)..(591).  
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Best Local Similarity 80.3%; Pred. No. 3.6e-67;  
Matches 362; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 37 CTTCCCTTCCCGCAACCTGGGATGAATCTCCACAGTGTGGTTCCTTTGGCTCCT 96  
DB 144 CCCCCTGGCTACTCCCGCAGATGAACCTCCATTCGCTGGCTTGGCTTGGCTCCT 203  
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DB 384 GAAGCTGGGCTGTGAGCCCAACTGGAAGATATCTTTCTGTGTCAGCGAAGCTGGCAT 443  
QY 337 TTTCTGCGCGGAGACCACTGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396  
DB 444 CTTCTGTGTGTAGAACCGGCTTGCAGCGGATACCTGCGAGTGTGACAGAGAGCTGC 503  
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QY 457 GCTGTGACCGGGCCACCGGCTGCTGA 487  
DB 564 GCTGTGACTGGGCCCAACCCACCTTGTCTGA 594  
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AF112984 883 bp mRNA linear ROD 23-FEB-2000  
LOCUS AF112984  
DEFINITION Mus musculus secretory phospholipase A2 (Pla2) mRNA, complete cds.  
ACCESSION AF112984

AF112984.1 GI:6651396  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 883)  
AUTHORS Suzuki, N., Ishizaki, J., Yokota, Y., Higashino, K., Ono, T., Ikeda, M., Fujii, N., Kawamoto, K. and Hanasaki, K.  
TITLE Structures, enzymatic properties, and expression of novel human and mouse secretory phospholipase A(2)s  
J. Biol. Chem. 275 (8), 5785-5793 (2000)  
20145788  
PUBMED 10681567  
REFERENCE 2 (bases 1 to 883)  
AUTHORS Ishizaki, J., Suzuki, N., Higashino, K. and Hanasaki, K.  
TITLE Direct Submission  
JOURNAL Submitted (11-DEC-1998) Shionogi Research Laboratories, Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan  
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ORIGIN  
Query Match 63.4%; Score 308.6; DB 10; Length 883;  
Best Local Similarity 80.3%; Pred. No. 3.6e-67; Indels 0; Gaps 0;  
Matches 362; Conservative 0; Mismatches 89;  
QY 37 CTTCCCTTCCCGCAACCTGGGATGAATCTCCACAGTGTGGTTCCTTTGGCTCCT 96  
DB 144 CCCCCTGGCTACTCCCGCAGATGAACCTCCATTCGCTGGCTTGGCTTGGCTCCT 203  
QY 97 GGTGGCTGTGTCAACGGGAACCTGGTTCAGTTTGGGTTGATGATCGAGAGATGACAGG 156  
DB 204 GGTGCCCCCTGGTGGGGGAACCTGGTCCAGTTTGGAGTGTATGAGAGAAATGACCGG 263  
QY 157 CAACTCCGCTCCAGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216  
DB 264 AAAGCTGGCTGGAGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323  
QY 217 GCGGTGGACCACTGACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276  
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DB 384 GAAGCTGGGCTGTGAGCCCAACTGGAAGATATCTTTCTGTGTCAGCGAAGCTGGCAT 443  
QY 337 TTTCTGCGCGGAGACCACTGCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396  
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QY 397 CTTCTGCTTGGCGCAACTGCGGACCTTACACCGCAATATGCCATATATCCCAACAA 456  
DB 504 TCTTTGCTTGGCGCAACTGCGGACCTTACACCGCAATATGCCATATATCCCAACAA 563  
QY 457 GCTGTGACCGGGCCACCGGCTGCTGA 487  
DB 564 GCTGTGACTGGGCCCAACCCACCTTGTCTGA 594

Db 564 GCTGTACTGGGCCACCCACCCTGCTGA 594

RESULT 10  
E37217  
LOCUS  
DEFINITION Gene encoding novel mouse secretory phospholipase A2.  
ACCESSION E37217  
VERSION E37217.1 GI:18626627  
KEYWORDS JP 2000166568-A/1.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Ishizaki, J., Suzuki, N. and Hanasaki, K.  
TITLE Gene encoding novel mouse secretory phospholipase A2  
JOURNAL Patent: JP 2000166568-A 1 20-JUN-2000;  
SHIONOGI & CO LTD

COMMENT  
OS Mus musculus (mouse)  
PN JP 2000166568-A/1  
PD 20-JUN-2000  
PF 09-DEC-1998 JP 1998349604

PR JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI  
PI C12N15/09, C07K16/40, C12N5/10, C12N9/16, C12Q1/44// (C12N15/09, PC  
C12R1:91),  
PC (C12N5/10, C12R1:91), (C12N9/16, C12R1:91), (C12N15/00, C12N5/00, PC  
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QY 265 CGGCGGCTGGAGAGCTGGGCTGTGAGCCAAACTGGAAAAGTATCTTTCTCTGTGCTAG 324  
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QY 385 CAAGAGGGCTGCCCTCTGCTTTGCGCGCAACCTGGGACCTCAACCGCAAAATATGCCA 444  
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QY 445 TTATCCCAACAGCTGT 461  
Db 304 CTACCCCAACAGCTGT 320

RESULT 11  
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LOCUS  
DEFINITION A gene encoding novel human secretory type phospholipase A2.  
ACCESSION BD013128.1 GI:22093317  
VERSION WO 0121775-A/1.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Ishizaki, J., Suzuki, N. and Hanasaki, K.  
TITLE A gene encoding novel human secretory type phospholipase A2  
JOURNAL Patent: WO 0121775-A 1 29-MAR-2001;  
SHIONOGI & CO LTD, JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI

COMMENT  
OS Mus musculus (mouse)  
PN WO 0121775-A/1  
PD 29-MAR-2001  
PF 18-SEP-2000 WO 2000JP006344  
PR 21-SEP-1999 JP 99P 266616  
PI JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI  
PC C12N5/20, C12N15/55, C12P21/02, C12P21/08, C07K16/40 CC  
FH Key Location/Qualifiers  
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ORIGIN  
Query Match 39.1%; Score 190.4; DB 6; Length 320;  
Best Local Similarity 78.5%; Pred. No. 2.4e-37;  
Matches 249; Conservative 0; Mismatches 66; Indels 2; Gaps 2;  
QY 146 AAGATGACAGGCAAGTCCGCTCGAGTACACGACTATGGTGTTACTGGCGCATCGGT 205  
Db 5 AAGAGANGAGGGAACCTGCCCTGNAGTACAAATNACTATGGTGCTATTGGGTGCGGT 64  
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Db 304 CTACCCCAACAGCTGT 320

RESULT 12  
AL358253/c  
LOCUS  
DEFINITION Human DNA sequence from clone RP11-460G22 on chromosome 1, complete  
sequence.  
ACCESSION AL358253  
VERSION AL358253.16 GI:23304623  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Bagguley, C.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On Sep 23, 2002 this sequence version replaced gi:22797900.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr1  
 RP11-460G22 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm

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Query Match 29.6%; Score 144; DB 9; Length 101824;  
 Best Local Similarity 100.0%; Pred.No. 1.5e-25;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 344 GCGGCGAGGACACCTGCGAGGCTGACCTGCGAGGTGACAGAGGCTGCCCTCTGC 403  
 Db 13902 GCGGCGAGGACACCTGCGAGGCTGACCTGCGAGGTGACAGAGGCTGCCCTCTGC 13843  
 QY 404 TTTCGCCGCAACCTGGGCACTTACACCGCAATATGCCATTATCCCAACAGCTGTGC 463  
 Db 13842 TTTCGCCGCAACCTGGGCACTTACACCGCAATATGCCATTATCCCAACAGCTGTGC 13783  
 QY 464 ACCGGGCGCCACCCCGCTGTCTGA 487  
 Db 13782 ACCGGGCGCCACCCCGCTGTCTGA 13759

## RESULT 13

AL360079/c 157470 bp DNA linear HTG 10-JUL-2001  
 LOCUS  
 Homo sapiens chromosome 1 clone RP11-66M4, 22 unordered pieces.  
 DEFINITION  
 ACCESSION AL360079  
 VERSION AL360079.3 GI:9801103  
 KEYWORDS HTG; HTGS\_PHAS51; HTGS\_CANCELLED.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Mclay, K.  
 Direct Submission  
 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone  
 requests: clonerequest@sanger.ac.uk  
 On Aug 14, 2000 this sequence version replaced gi:8919533.  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: BA6M4  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator ET-amersham; 1% of reads Chemistry:  
 Dye-terminator Big Dye; 98% of reads  
 Consensus quality: 145607 bases at least Q40  
 Consensus quality: 150854 bases at least Q30  
 Consensus quality: 153362 bases at least Q20  
 Insert size: 15370; sum-of-contigs  
 Insert size: 175968; 2.3% error; agarose-fp  
 Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality  
 coverage: 3.16x in Q20 bases; agarose-fp  
 -----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 22 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 15108: contig of 15108 bp in length  
 \* 15109: gap of 100 bp  
 \* 15208: gap of 100 bp  
 \* 15209: contig of 4869 bp in length  
 \* 20177: gap of 100 bp  
 \* 20178: contig of 6421 bp in length  
 \* 26598: gap of 100 bp  
 \* 26599: gap of 100 bp  
 \* 31874: contig of 5176 bp in length  
 \* 31875: gap of 100 bp  
 \* 31975: contig of 7606 bp in length  
 \* 39580: gap of 100 bp  
 \* 39581: contig of 23297 bp in length  
 \* 62978: gap of 100 bp  
 \* 63078: contig of 12577 bp in length  
 \* 75654: gap of 100 bp  
 \* 75755: contig of 14913 bp in length  
 \* 90667: gap of 100 bp  
 \* 90668: gap of 100 bp  
 \* 90767: gap of 100 bp  
 \* 93945: contig of 3178 bp in length  
 \* 94045: gap of 100 bp  
 \* 94046: contig of 4977 bp in length  
 \* 99022: gap of 100 bp  
 \* 99023: contig of 2577 bp in length  
 \* 99123: contig of 100 bp  
 \* 101699: gap of 100 bp  
 \* 101799: contig of 3442 bp in length  
 \* 101800: gap of 100 bp  
 \* 105241: contig of 2197 bp in length  
 \* 105242: gap of 100 bp  
 \* 105342: contig of 2197 bp in length  
 \* 107538: gap of 100 bp  
 \* 107539: contig of 3370 bp in length  
 \* 107638: gap of 100 bp  
 \* 111008: contig of 2647 bp in length  
 \* 111109: gap of 100 bp  
 \* 111756: contig of 100 bp  
 \* 113856: gap of 100 bp  
 \* 113857: contig of 7441 bp in length  
 \* 121297: gap of 100 bp  
 \* 121396: contig of 4445 bp in length  
 \* 125841: contig of 100 bp  
 \* 125842: gap of 100 bp  
 \* 125942: contig of 3315 bp in length  
 \* 129257: gap of 100 bp  
 \* 129356: contig of 100 bp  
 \* 129357: contig of 6913 bp in length  
 \* 136269: gap of 100 bp  
 \* 136270: contig of 2510 bp in length  
 \* 136369: gap of 100 bp  
 \* 136370: contig of 2510 bp in length

\* 138880 138979: gap of 100 bp  
 \* 138980 144504: contig of 5525 bp in length  
 \* 144505 144604: gap of 100 bp  
 \* 144605 157470: contig of 12866 bp in length.

## FEATURES

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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
 /clone="RP11-66M4"  
 /clone\_lib="RPCT-11.1"

## misc\_feature

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 /note="assembly\_fragment:00413"  
 clone\_end:SP6  
 vector\_side:left  
 15209..20077

## misc\_feature

/note="assembly\_fragment:00153"  
 20178..26598

## misc\_feature

/note="assembly\_fragment:00168"  
 26699..31874

## misc\_feature

/note="assembly\_fragment:00204"  
 31975..39580

## misc\_feature

/note="assembly\_fragment:00207"  
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## misc\_feature

/note="assembly\_fragment:00211"  
 63078..75654

## misc\_feature

/note="assembly\_fragment:00223"  
 75755..90667

## misc\_feature

/note="assembly\_fragment:00330"  
 90768..93945

## misc\_feature

/note="assembly\_fragment:00333"  
 94046..99022

## misc\_feature

/note="assembly\_fragment:00365"  
 99123..101699

## misc\_feature

/note="assembly\_fragment:00421"  
 101800..105241

## misc\_feature

/note="assembly\_fragment:00566"  
 105342..107536

## misc\_feature

/note="assembly\_fragment:00589"  
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## misc\_feature

/note="assembly\_fragment:00674"  
 111109..113755

## misc\_feature

/note="assembly\_fragment:00850"  
 113856..121296

## misc\_feature

/note="assembly\_fragment:01043"  
 121397..125841

## misc\_feature

/note="assembly\_fragment:01136"  
 125942..129256

## misc\_feature

/note="assembly\_fragment:01206"  
 129357..136269

## misc\_feature

/note="assembly\_fragment:01276"  
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## misc\_feature

/note="assembly\_fragment:01282"  
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## misc\_feature

/note="assembly\_fragment:01387"  
 144605..157470

/note="assembly\_fragment:01404"

## ORIGIN

Query Match 29.6%; Score 144; DB 2; Length 157470;

Best Local Similarity 100.0%; Pred. No. 1.5e-25;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 GCGGCGAGGACCACTGCGAGGGTGCACCTCGAGTGTGACAGAGGGCTGCCCTGCG 403

|||||GCGGCGAGGACCACTGCGAGGGTGCACCTCGAGTGTGACAGAGGGCTGCCCTGCG 27263

Db 27322 GCGGCGAGGACCACTGCGAGGGTGCACCTCGAGTGTGACAGAGGGCTGCCCTGCG 463

|||||TTTCCCGCAACTGGGCACTTACACCGCAATATGCCCAATATGCCCAAGCTGTGC 27203

QY 27262 TTTCCCGCAACTGGGCACTTACACCGCAATATGCCCAATATGCCCAAGCTGTGC 463

|||||TTTCCCGCAACTGGGCACTTACACCGCAATATGCCCAATATGCCCAAGCTGTGC 27203

Db 27262 TTTCCCGCAACTGGGCACTTACACCGCAATATGCCCAATATGCCCAAGCTGTGC 463

|||||TTTCCCGCAACTGGGCACTTACACCGCAATATGCCCAATATGCCCAAGCTGTGC 27203

QY 464 ACCGGGGCCACCCCGCCCTGTGTA 487

Db 27202 ACCGGGGCCACCCCGCCCTGTGTA 27179

## RESULT 14

## AC116054

## LOCUS

## DEFINITION

## AC116054

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Rattus norvegicus

## Rattus norvegicus

## Rattus norvegicus

## Rattus norvegicus

## Rattus norvegicus

## Rattus norvegicus

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## Rattus norvegicus

Db	111622	TTTCGCCACAACTGGGCACTTATAACCGCAAGTATGCTCACTACCCCAACAACTGTGC	111681
Qy	464	ACGGGGCCCAACCGCCCTGCTGA	487
Db	111682	ACTGGGCCCAACCCACCTGCTGA	111705
RESULT 15			
AC118094/c			
LOCUS	AC118094	282515 bp	DNA linear HTG 15-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-117D17, WORKING DRAFT SEQUENCE, 3 unordered pieces.		
ACCESSION	AC118094.6	GI:25009605	
VERSION	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.		
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 282515)		
AUTHORS	Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Crear, A., Dederich, D., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, S., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Guarnate, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, J., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, B., Jacob, L., Jiang, H., Johnson, B., Johnson, K., Joive, A., Kapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulised, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, K., Martinez, B., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, N., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, N., Sutton, A., Svatek, A., Tabors, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weinstock, G., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs R.A.		
	Direct Submission		
	Unpublished		
TITLE	JOURNAL		

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 239739)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24942319.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: G3EO

Center clone name: CH230-38C10

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 219221 bases at least Q40

Consensus quality: 222773 bases at least Q30

Consensus quality: 225047 bases at least Q20

Estimated insert size: 229739; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* Location/Qualifiers

1. 239739

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-38C10"

160857..162689

/note="wgs\_contig"

/complement(238368..237160)

/note="clone\_boundary"

clone\_end:T7

site:EcoRI

end\_sequence:BH308572"

ORIGIN

Query Match 23.7%; Score 115.2; DB 2; Length 239739;

Best Local Similarity 87.5%; Pred. No. 2.8e-18;

Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 344 CGCGCAGACCACTGCGGCGTACCTGCGGAGTGTGACAGAGGGTGGCCCTGTC 403

Db 111562 CTGTGTGAAGCACTTGCACGGCGCAGACCTGTGTGTGTGACAGAGTGGCCCTGTC 111621

Qy 404 TTTCGCCCAACCTGGGCACTTATAACCGCAATATGCCCACTTATCCCAACAGCTGTGC 463



REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 282515)  
Worley,K.C.  
Direct Submission  
Submitted (13-APR-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 282515)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 15, 2002 this sequence version replaced gi:23265558.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GUXU  
Center clone name: CH230-117D17

----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 255167 bases at least Q40  
Consensus quality: 258594 bases at least Q30  
Consensus quality: 260981 bases at least Q20  
Estimated insert size: 261710; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html)  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
consists of 3 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

\* 1 221138: contig of 221138 bp in length  
\* 221139 221238: gap of unknown length  
\* 221239 280772: contig of 59534 bp in length  
\* 280773 280872: gap of unknown length  
\* 280873 282515: contig of 1643 bp in length.

FEATURES  
source

Location/Qualifiers  
1. .282515  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-117D17"  
330. .81776  
/note="clone boundary"  
clone\_end:17  
site:

misc\_feature

end\_sequence:BH279848"  
6087. .6517  
/note="clone boundary"  
clone\_end:Sp6  
site:  
end\_sequence:BH279850"

misc\_feature

misc\_feature 221239. .222784  
/note="wgs end\_extension  
clone\_end:Sp6"

ORIGIN

Query Match 23.7%; Score 115.2; DB 2; Length 282515;  
Best Local Similarity 87.5%; Pred. No. 2.8e-16;  
Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 344 CCGCGCAGGACCCTGCGCAGCGCTGACCTGCGAGTGTGACACAGAGGGTGCCTCTGC 403  
Db 246335 GCTGGTAGAAGCACTTCCAGCGCGACCTGTGAGTGTGACACAGAGTGCCTCTGC 246276  
QY 404 TTTCGCGCAACCTGGGCACCTACACCGCAATATGCCATTATCCCAACAGCTGTGC 463  
Db 246275 TTTCGCCACACCTGGGCACTTATACCGCAAGTATCTACTACCCCAACAACTGTGC 246216  
QY 464 ACCGGGCCCAACCCCGCCCTGTGTA 487  
Db 246215 ACTGGGCCCAACCCCGCCCTGTGTA 246192

Search completed: November 13, 2004, 05:43:02  
Job time : 1701 secs

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